us-09-385-918-3.rai

Run on:

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100.0%; Score 218; DB 3;
100.0%; Pred. No. 1.5e-21;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 38; Conservative
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MOLECULE TYPE: protein
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Sequence 6
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-08-610-916A-18
US-08-610-916A-11
US-08-655-912A-11
US-08-630-916A-17
US-08-630-916A-17
US-08-476-598-13
US-08-476-598-13
US-08-55-912A-6
US-08-55-912A-6
US-08-630-916A-36
US-08-630-916A-36
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US-08-630-916A-35
US-09-774-639-371
US-09-919-039-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513545 segs, 74649064 residues
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GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
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Perfect score:
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Maximum DB
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Result . 8

Sequence 4, Appli Sequence 4, Appli Sequence 1186, A Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 32, Appl Sequence 32, Appl Sequence 12, Appl Sequence 12, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 24, Appl Sequence 26, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli US-08-895-601-6
| Sequence 6, Application US/08895601
| Sequence 6, Application US/08895601
| Patent No. 6060262| GENERAL INFORMATION:
| APPLICANT: Beer-Romero, Peggy
| APPLICANT: Glass, Susan J. APPLICANT: Rolfe, Mark
| TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,
| TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: FOLEY, HOAG & ELIOT LLP
| STREET: One Post Office Square Sequence COMPUTEY: PLA

COMPUTEY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIAN COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIAN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,601
FILING DATE: 16-JUL-1997
CLASSIFICATION WHER: 36,709
REFERENCY/CATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REFERENCY/CATION NUMBER: MIV-096.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-832-7000
STELEFAX: 617-832-7000
TELEFAX: 617-832-7000
STELEFAX: 617-832-7000 US-09-070-060-3 US-09-357-746-3 US-09-0157-746-4 US-09-157-746-4 US-09-157-746-4 US-09-157-746-4 US-09-1539-1638-4 US-08-1916A-4 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-630-916A-3 US-08-39-205A-2 US-08-30-916A-3 US-08-30-916A-3 US-08-30-916A-3 US-08-30-205A-2 US-08-30-205A-2 US-08-30-205A-2 ALIGNMENTS 

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Gaps

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Length 927; Indels

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PatentIn Release #1.0, Version #1.30
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USA
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                                                                                                                                                          APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: DENTFECATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
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Pred. No. 6.2e-22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                               SIREE:: New York

CTTY: New York

STATE: New York

COMPUTER: New York

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,916A

FLING DATE: 03-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGRYI INFORMATION:

NAME: MISSOCK, S. LESLER

REGISTRATION NUMBER: 1101-203

TELECOMMUNICATION NUMBER: 1101-203

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAX: (212) 790-9090

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CRARACTERISTICS:

LENGTH: 38 amino acids
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Patent No. 5952467

GENERAL INFORMATION:
APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                           Sequence 18, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.9%;
ilarity 97.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-630-916A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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Matches 37; Conserv
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Gaps
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APPLICATION NUMBER: US/08/555,912A FILING DATE: U3-NOV-1995 CLASSIFICATION: 435 ATTONEY AGENT INPORMATION:
NAME: Hailb. Lisa A REGISTRECE/DOCKET NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07251/011001 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 150509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
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TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                        PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA: US/09/066,074

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08555912A
Patent No. 5972697
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not relevant
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Best Local Similarity 89.5'
Matches 34, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 IOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nedd4/Mouse
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A SH2 DOMAIN ASSOCIATED PROTEIN, A SIGNALLING DOWAIN THEREIN, NUCLBIC ACIDS ENCODING THE PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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Sequence 13, Application US/08476509B
Sequence 13, Application US/08476509B
Sequence 13, Application US/08476509B
Sequence 13, Application US/08476509B
Sequence 13, Application CO4412
Repert No. CO4412
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALLING DOMAIN THERIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: U1-DEC-1994
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1487-5800
TELEFAX: 201 343-1684
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Pred. No. 4.2e-21;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: A SH2 DOMAIN
TITLE OF INVENTION: SIGNALLING DO
TITLE OF INVENTION: PROTEIN AND TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                         STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 Hackensack Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.5%;
Matches 34; Conservative 3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .. protein
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mouse-1
IMMEDIATE SOURCE:
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COUNTRY: USA
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-348-518C-13
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Sequence 17, Application US/08630916A

Patent No. 6011137

GENERAL INFORMATION:

APPLICANT: BLOAZE, Gregorio

APPLICANT: RAy, Brian K.

TITLE OF INVENTION: DEWRIFTCATION AND ISOLATION OF NOVEL

TITLE OF INVENTION: DOLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 124

CONTRESPONDENCE ADDRESS;

ADDRESSEE: Pennie & Edmonds

STREE: 1155 Avenue of the Americas

CITY: New York

COUNTRY: United States

ZIP: 10036-2711

COUNTRY: United States

ZIP: 10036-2711

COMPUTER: IBM PC Compatible

OPERATION TYPE: Ploppy disk

COMPUTER: DAPPLICATION NATA:

MEDILOATION NATE: PLOPPY DEAP

ATTORNER'S APPLICATION NATE: 10, Version #1.30

CLASSIFICATION: AS LESLIE

REGISTRATION NUMBER: 10, 096630, 916A

ATTORNER'S APROPER'S LIB STATE: 10, 097909090

TELEPRATION TOWNER: 10, 0969630, 910A

TELECHONE: (212) 790-9090

TELECHONE: (212) 790-9090

TELECHONE: (212) 790-9090

TELECHONE: CARRACTERSTICS: 1786

SEQUENCE CHARACTERSTICS: 1786

SECUENCE CHARACTERSTICS: 1786

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                                                                                                                 Length 38;
                                                                                                                                                                        1; Indels
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89.5%; Pred. No. 4.2e-21;
tive 3; Mismatches 1;
                                                                                                              Score 203; DB 2;
Pred. No. 4.2e-21;
3; Mismatches 1.
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Patent No. 6022740
GENERAL INFORMATION:
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
                                                                                                                 93.1%;
89.5%;
                                                                                            Query Match
Best Local Similarity 89.5'
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 38 amino acids
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Matches 34; Conservative
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Nedd4/Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-08-348-518C-13
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US-08-630-916A-17
                                                       US-08-555-912A-11
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US-08-539-205A-6
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Sequence 36, Application US/09252404A

Patent No. 6495376

GENERAL INFORMATION:
APPLICANT: Kun Ping Lu
APPLICANT: Xiao Zhen Zhou
ITILE OF INVENTION: Methods and Compositions for Regulating
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 1440.1034.000
CURRENT APPLICATION NUMBER: US/09/252,404A

CURRENT FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 42

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 36

LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
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89.5%; Pred. No. 4.2e-21;
iive 3; Mismatches 1
                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Jackson Esg., David A.
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMINICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 208 SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 aming acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGWENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mouse-1
IMMEDIATE SOURCE:
CLONE: Nedd4
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-476-509B-13
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Sequence 6, Application US/08539205A
Patent No. 6001619
GENERAL INFORMATION
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES.
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89.5%; Pred. No. 4.2e-21;
tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                    ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/275,900
FILING DATE: 24-Mar-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: Nedd4/Mouse
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.5<sup>5</sup>
Matches 34; Conservative
                                                                                                                                                 CITY: La Jolla
                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cliant
STATE: Par
COUNTRY: USA
TP: 02109-2170
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APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13

US-08-630-916A-20

J. Sequence 2.0. Application US/08630916A

J. Sequence 2.0. Application US/08630916A

J. September 2.0. Application US/08630916A

J. Seneral Information:

J. APPLICANT: Fowlkes, Dana M.

TITLE OF INVENTION: DELVIPERTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

TITLE OF INVENTION: POLYPERTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

J. CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

STREET: New York

STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
                                           73 PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.1%; Score 142; DB 3; 67.6%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PLPPGWEKRQDVNGRVYYVNHNTRITQWEDPRTQ 35
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            2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD
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                                                                                                                                                                             Sequence 16, Application US/08630916A; Patent No. 6011137; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: United States
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.6
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                              US-08-630-916A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.9%; Score 148; DB 3; Length 83
Best Local Similarity 71.4%; Pred. No. 6e-12;
Matches 25; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQD 36
APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-0CT-1995
ATTORNEY/ACBNT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1000
TELEFAX: (617) 832-1000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09392163A
Patent No. 6503742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-1000
INFORMATION FOR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 834 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 71.4
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                            US-08-539-205A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-392-163A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-392-163A-6
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A SH2 DOMAIN ASSOCIATED PROTEIN, A SIGNALLING DOMAIN THERRIN, NUCLEIC ACIDS ENCODING THE PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.3%; Score 138; DB 3; Length 38; 62.2%; Pred. No. 3.9e-12; ive 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REJERENCE/DOCKET NUMBER: 26,742
REJERENCE/DOCKET NUMBER: 26,742
RELEFENCE/DOCKET UNBER: 36,742
RELEFENCE CHARACTERISTICS:
LEMETAN: 201 437-1684
TELEFY: 201 343-1684
TELEFY: 301 343-1684
TELEFY: 38 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: TIDEACTERISTICS:
LEMGTH: 38 amino acids
TOURDOCY: Innear
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Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SIGNALLING DOMAIN
TITLE OF INVENTION: SIGNALLING DOMAIN
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3%;
Best Local Similarity 62.2%;
Matches 23; Conservative
                                                                        38 amino acids
                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mouse-2
IMMEDIATE SOURCE:
CLONE: Nedd4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO FRAGMENT TYPE: ir ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
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                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                        LENGTH:
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Sequence No. 602240

GENERAL INFORMATION:

APPLICANT: SUDOL, MARIUS

APPLICANT: HENRY, CHEN

TITLE OF INVENTION: A SIGNALLING DOWAIN THEREIN, NUCLEIC ACIDS ENCODING THE

TITLE OF INVENTION: PROTEIN AND THE DOWAIN, AND DIAGNOSTIC AND THERAPEUTIC USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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62.2%; Pred. No. 3.9e-12;
live 6; Mismatches 8; Indels
                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FLING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LEGLIE
REGISTRATION NUMBER: 1101-203
TELEPAN: (212) 790-990
TELEPAN: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acid
TYPE: MINDONESS:
COMPUTER REPERENTING ACID
TYPE: MINDONESS:
COMPUTER REPERENTING
TYPE: MINDONESS:
COMPUTER REPERENTING
TYPE: MINDONESS:
COMPUTER REPERENTING
TYPE: MINDONESS:
COMPUTER REPERENTING
TYPE: MINDONESS:
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.27
...rhes 23; Conservative
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: peptide US-08-630-916A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201 (TELEX: 133521
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US-08-348-518C-14
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Query Match 63.3%; Score 138; DB 3; Length 38; Best Local Similarity 62.2%; Pred. No. 3.9e-12; Matches 23; Conservative 6; Mismatches 8; Indels
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Search completed: October 13, 2005, 14:03:04 Job time : 18.2202 secs

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Sequence 2, Appli Sequence 17, Appl Sequence 17, Appl Sequence 371, Appl Sequence 335, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 15, Appli Sequence 11, Appl Sequence 16, Appl

Run on:

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APPLICANT: FOWLES, Gregorio
APPLICANT: FOWLES, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMULICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 796-8064/9741
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
US-08-348-518C-2
US-08-630-916A-22
US-08-476-509B-17
US-09-774-639-371
US-09-919-039-235
US-09-919-039-235
US-09-319-046-3
US-09-357-746-3
US-09-357-746-4
US-09-357-746-4
US-09-357-746-4
US-08-630-916A-15
US-08-630-916A-15
US-08-630-916A-16
US-08-476-509B-11
US-08-476-509B-11
US-08-430-916A-6
US-08-539-205A-6
US-09-392-205A-6
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Pred. No. 1.6e-10;
0; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States
ZIP: 10036-2711
COMPUTER READBALE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/08630916A Patent No. 6011137 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53:1%;
Matches 17; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
 MOLECULE TYPE: peptide
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                                                                                                                        October 13, 2005, 13:50:53; Search time 15.7143 Seconds (without alignments) 156.763 Million cell updates/sec
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Compugen Ltd.
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US-09-270-767-59345
US-09-270-767-59345
US-08-630-916A-39
US-08-630-916A-26
US-08-348-518C-18
US-08-348-518C-18
US-08-39-205A-4
US-08-39-205A-4
US-08-630-916A-48
US-08-630-916A-48
US-08-630-916A-48
US-08-630-916A-19
US-08-630-916A-19
US-08-630-916A-19
US-08-630-916A-19
US-08-630-916A-19
US-08-630-916A-14
US-08-630-916A-16
US-09-275-900-12
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-630-916A-16
US-08-348-518C-12
US-08-348-518C-12
US-08-448-518C-5
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                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                     GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
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                                      Copyright
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                                                                                                                                                                                                                                                                             Scoring table:
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Maximum DB
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Length 38; Indels

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LOCATION: 12
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS:
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APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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Sequence 59345, Application US/09270767

Sequence 503491

Batent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVEXTION:
NUCLER REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NOWHER OF SEQ ID NOS: 62517

SEQ ID NO 59345

LENGTH: 158
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43942
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Pred. No. 5.7e-09;
1; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
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Pred. No. 1.8e-09;
1; Mismatches 15
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                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-59345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43942
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50.0%;
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Best Local Similarity 50.0%;
Matches 16; Conservative
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Best Local Similarity 50.09
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New York
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US-08-630-916A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A Hydrophobic Amino Acid."
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
LOCATION: 25
OTHER INFORMATION: /note= "A Hydrophobic Amino Acid.
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid.
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note= "A Hydrophobic Amino Acid
                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A FILING DATE: 03-APR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "A Polar Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93; DB 3; 1 Pred. No. 7.3e-10;
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                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 14
OTHER INFORMATION: /note=
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70.08;
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LOCATION: 16
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Best Local Similarity 70.0
Marches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     33 amino acids
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A SH2 DOMAIN ASSOCIATED PROTEIN, A SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: REALBLE FORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: 01-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101
TELECOMMUNICATION INFORMATION:
TELEFAX: 201343-1684
                                                                    CURRENT APPLICATION PAPER

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 435
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MISROCK, S. LEGLIE
REGISTRATION NUMBER: 1101-203
TELEFANCE/DOCKET NUMBER: 1101-203
TELEFANCE/DOCKET NUMBER: 1101-203
TELEFANCE/DOCKET NUMBER: 1203
TELEFANCE/DOCKET NUMBER: 1203
TELEFANCE/DOCKET NUMBER: 1203
TELEFANCE/DOCKET NUMBER: 130-9090
TELEFANCE/DOCKET NUMBER: 120-9090
TELEFANCE/DOCKET NUMBER: 120-9090
TELEFANCE/DOCKET NUMBER: 120-9090
TELEFANCE/DOCKET NUMBER: 120-9090
TELEFANCE (212) 996-8864/9741
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 92; DB 3; 1
Pred. No. 1.3e-09;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PLPPGWEKRTDPRGRFYYVDHNTRTTTWORP 32
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08348518C
Patent No. 6022740
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
71.3%;
Best Local Similarity 51.6%;
Matches 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: SIGNALI
TITLE OF INVENTION: PROTEII
TITLE OF INVENTION: PROTEII
TITLE OF INVENTION: THEREO
TITLE OF INVENTION: THEREO
TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jaci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: peptide
US-08-630-916A-35
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
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                                                                       US-08-630-916A-26

Sequence 26, Application US/08630916A
Sequence 26, Application Information Companies Information US/08630916A
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PINOZZI, Gregorio
APPLICANT: Ray, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CUNTRY: United States
ZIP: 10036-271

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION ADAR: 03-APR-1996
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 1101-203
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GPLPXGWEXXXXXXXXXXXYXXHNTXTTXWXXP 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-630-916A-26
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                                                      RESULT 5
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Gaps ..

Length 38; 15; Indels .. 0

Gaps

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Sequence 4, Application US/08539205A
Patent No. 6001619
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09392163A
Patent No. 6503742
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%; Score 92; DB 3; Length 766;
46.9%; Pred. No. 3.7e-08;
tive 1; Mismatches 16; Indels
Indels
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Parentin Release #1.0, Version #1.30
SOFTWARE: Parentin Release #1.0, Version #1.30
SOFTWARE: Parentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,205A
FTILIG DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 26V-005.01
FREFERENCE/DOCKET NUMBER: CSV-005.01
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-1000
TELEFAX: (617) 832-7000
TELEFAX: (617) 832-1000
TELEFAX: (617) 832-7000
16;
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                                           1 GPLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
1; Mismatches
                                                                                       1 GPLPSGWEMRLINTARVYFVDHNTKTTTWDDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.9
Matches 15; Conservative
15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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US-09-392-163A-4
Matches
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APPLICANT: PEER, BORK
TITLE OF INVENTION: STGNALLING DOWAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: STGNALLING DOWAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: PROTOEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
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Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                      Length 38;
                                                                                                                                                                                                                                                                                                    16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: 201487-5800
                                                                                                                                                                                                                                                    Score 92; DB 3;
Pred. No. 1.3e-09;
1; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                  1 GPLPXGWEXXXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                           1 GPLPSGWEMRLINTARVYFVDHNTKTTTWDDP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-509B-18; Sequence 18, Application US/08476509B; Patent No. 6034212; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 amino acids
                                      MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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IMMEDIATE SOURCE:
                                                                                                                                    ORGANISM: Yeast-3
IMMEDIATE SOURCE:
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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Best Local Similarity
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ORIGINAL SOURCE:
                                                                                                                                                                                , CLONE: Rsp5
US-08-348-518C-18
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US-08-476-509B-18
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                                                                                                                  71.3%; Score 92; DB 3; Length 906; 51.6%; Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
                                                                                                                                                            15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,074
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 70.5%; Score 91; DB 2; Le Best Local Similarity 50.0%; Pred. No. 1.9e-09; Matches 16; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 PLPPGWEKRTDPRGRFYVVDHNTRTTTWQRP 397
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                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                      2 PLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALLOMANDA MAIN MARKE 188 A. REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION 189678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: -13-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08555912A; Patent No. 5972697; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09066074 Patent No. 5952467 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                      Local Similarity 51.6
nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPE
OPERATING SYSTEM: PC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                             TOPOLOGY: unknown MOLECULE TYPE: peptide US-08-630-916A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSP5/SC
           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-066-074-12
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                                                                                                                    Query Match
                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pirozi, Gregorio
APPLICANT: Ray, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Ray, Brian K.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
COWTRY: United States
CIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/392,163A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GPLPXGWEXXXXXXXXXXYXXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELEPOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101-203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 796-8064/9741
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          : 766 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 906 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-08-630-916A-48
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Sequence 38, Application US/08630916A

Patent No. 601137
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: First Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 1.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPER FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
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                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLOWING TO THE REGISTRATION NUMBER: 18,972
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.5%;
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Best Local Similarity 46.91
Matches 15; Conservative
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                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS:
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STRANDEDNESS:
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Matches 16; Conserv
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US-08-630-916A-19

US-08-630-916A-19

Sequence 19, Application US/08630916A

Sequence 19, Application US/08630916A

Patent No. 6011137

GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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COMPARY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Flogpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILLING DATE: 03-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  SCHWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-NOV-1995 CLASSIFICATION: 435
  APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
ADDRESSEE: Fish & Richardson P.C.
                                                                                ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRLPPGWERRTDNFGRTYYVDHNTRTTTWKRP 32
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                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                              COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: RSP5/SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-555-912A-12
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1 GPLPENWEMAYTENGEVYFIDHNTKTTSWLDP 32

Search completed: October 13, 2005, 14:03:04 Job time: 15.8393 secs

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5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2005

Copyright

- protein search, using sw model

OM protein

October 13, 2005, 14:01:04; Search time 243.297 Seconds (without alignments) 171.684 Million cell updates/sec Run on:

US-09-385-918-1 271 score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* geneseqp2000s:\*geneseqp2001s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp20048:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Add15147 Human 503	Aab83016 Human HEC	Aau87301 Novel cen		Adi54616 Novel hum	Aaw13384 Human pro	Aab31477 Amino aci	Adn95750 Human BEC		Adn05464 Antipsori		Adp54729 Human PRO	-	Aaw13387 Fission y	Ade31153 Human dia	Ads11077 Human the	Ade78997 Human pro	Aaw13385 Human pro	Abg70126 Human pre	Abg70111 Human pre	_		Abb63723 Drosophil	Aae05495 Human ubi	Aae32722 Nedd-4-li
ΩI	ADD15147	AAB83016	AAU87301	ADM20055	ADI54616	AAW13384	AAB31477	ADN95750	AAU19610	ADN05464	ABU70611	ADP54729	ADE62087	AAW13387	ADE31153	ADS11077	ADE78997	AAW13385	ABG70126	ABG70111	ADJ68961	ADO44003	ABB63723	AAE05495	AAE32722
DB	7	4	4	4	æ	7	4	7	4	œ	9	σ	7	N	7	œ	7	~	2	2	7	80	4	4	9
% Query Match Length DB	358	108	514	514	514	748	748	748	804	831	156	308	310	804	2044	2309	4374	766	1094	1488	2011	2011	5002	870	870
% Query Match	7.13	48.3	46.9	46.9	46.9	46.9	46.9	46.9	46.9	46.9	46.1	46.1	46.1	46.1	46.1	46.1	46.1	45.6	45.0	45.0	45.0	45.0	44.6	44.5	44.5
Score	140	131	127	127	127	127	127	127	127	127	125	125	125	125	125	125	125	123.5	122	122	122	122	121	120.5	120.5
Result No.	7	2	٣	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adq19348 Human sof	Tumour	Aaw36795 Novel hum	Adb49242 Novel hum	Aau23363 Novel hum	~	Aae32728 KIAA0317		Aab31476 Amino aci		Aabs0048 Human clo	Adc26289 Human NOV	Human	Abb05708 Human sig	Human	Abb59631 Drosophil	Abb59856 Drosophil	Amino	Adb47966 Novel hum	Adj55521 Novel hum
ADQ19348	ABM81770	AAW36795	ADB49242	AAU23363	ABP98335	AAE32728	AAE32724	AAB31476	ABB61120	AAB50048	ADC26289	AAB50049	ABB05708	ADS00021	ABB59631	ABB59856	AAY10943	ADB47966	ADJ55521
æ	œ	~	7	4	9	9	9	4	4	4	7	4	ß	ω	4	4	~	7	80
870	870	906	906	515	823	823	722	723	1035	733	868	922	922	930	949	949	474	474	474
44.5	44.5	44.5	44.5	44.3	44.3	44.3	44.1	44.1	43.9	43.7	43.7	43.7	43.7	43.7	43.4	43.4	43.0	43.0	43.0
120.5	120.5	120.5	120.5	120	120	120	119.5	119.5	119	118.5	118.5	118.5	118.5	118.5	117.5	117.5	116.5	116.5	116.5
56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

ADD15147 standard; protein; 358 AA. ADD15147

ADD15147;

15-JAN-2004 (first entry)

Human 50352 polypeptide E6-AP carboxyl terminus domain.

Human; ubiquitin-protein ligase 50352; neural tube defect; forebrain anomaly; posterior fossa anomaly; syringomyelia; colon tumour; cancer; creebrovascular disease; hypoxia; ischaemia; infarction; cellular proliferative disorder; cellular differentiative disorder; hormonal disorder; immune disorder; inflammatory disorder; uneurological disorder; blood vessel disorder; cytostatic; cardiant; vasotropic; endocrine; respiratory; antiinflammatory; neuroprotective; enzyme; E6-AP carboxyl terminus domain. 

Homo sapiens.

US2003100020-A1.

29-MAY-2003.

09-OCT-2002; 2002US-00268036. 09-OCT-2001; 2001US-0327820P.

(MILL-) MILLENNIUM PHARM INC.

Meyers RE;

WPI; 2003-787017/74.

Novel ubiquitin-protein ligase family member 50352 useful as diagnostic targets and therapeutic agent for controlling 50352 associated disorders such as neural tube defects, perinatal brain injury, hypoxia, ischemia.

Disclosure; SEQ ID NO 5; 53pp; English.

The invention relates to the human ubiquitin-protein ligase 50352 polypeptide and the polynucleotide encoding it. The polypeptide is useful for treating 50352-associated disorders such as neural tube defects, forebrain anomalies, posterior fossa anomalies, syringomyelia, colon tumours and cerebrovascular diseases such as hypoxia, ischaemia and infarction. The 50352 polypeptide and its modulators can act as therapeutic agents for controlling cellular proliferative and/or

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Query Match
48.3%; Score 131; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.8e-16;
Matches 85; Conservative 0; Mismatches 0;
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                                                                                                                264 WFWEIVEEFDKEERAKLLQFVTGSPRLPLQGFKSLEGSNGIPKFTIEKAGTEDERLPTAH 323
differentiative disorders, hormonal disorders, immune and inflammatory disorders, neurological disorders and blood vessel disorders. This sequence represents a human 50352 polypeptide E6-AP carboxyl terminus
                                                                                                                                                                                                                                                                          HECT E3 ubiquitin ligase, antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; againg; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis.
                                                                                              WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
                                                                                Gaps
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                                                                                                                                                                                                                                                                  Human; HECT; homologous to E6 carboxyl terminus; ubiquitination;
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                                                                                                                                                                                                                                                                                                                                                                                  amino acid, 0-1 residues may
                                                            Score 140; DB 7; Length 358;
Pred. No. 2e-17;
0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           0-3 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Met, Ala, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid"
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Xaa = any amino acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid"
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                                                                                                                                 TCFNXLDLPXYXSXXXXXXXXXX 101
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/note= "Xaa = any
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Val, Ile,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Val
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                                                                                                                                                                                                                                                                                                                                                                label= Tyr, Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Lys, Arg
                                                                                                                                                                                             AAB83016 standard; protein; 108
                                                                                                                                                                                                                                                  Human HECT consensus sequence.
                                                             51.7%;
37.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Thr,
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note= "Xaa
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                                                                              Conservative
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                                                                     Similarity
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                                            Sequence 358 AA;
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Matches 32; C
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The present sequence is a consensus HECT (homologous to E6 carboxyl terminus) sequence. A HECT sequence is found within the catalytic carboxyterminal domain of the HECT E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone to morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase who the cellular levels of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein by E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for treating cancer, Agents that inhibit TGF-mediated signalling are useful for treating cancer, that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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102. .107
//note= "Xaa = any amino acid, 0-2 residues may
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                                              = any amino acid, 0-6 residues may
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                                              'note= "Xaa
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/note= "Xaa
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note= "Xaa
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                                         WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXPXXH 76
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                  WFWXIXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
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2000US-018062B.
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421 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 480

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The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (II), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative clisorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. Alaheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. disphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallargic rhinitis, renal disorders e.g. capiratory disorders e.g. nonallargic rhinitis, renal disorders e.g. capiratory disorders e.g. nonallargic rhinitis, renal disorders e.g. capiratory disorders e.g. nonallargic rhinitis, renal disorders e.g. infarction. The polypeptides can also be used to aid wound healing and capiral organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or
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Pred. No. 7.8e-15;
3; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 819; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
             17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
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1-DEC-2000; 2000US-0250391P.
5-DEC-2000; 2000US-0251030P.
5-DEC-2000; 2000US-0251988P.
5-DEC-2000; 2000US-0256119P.
6-DEC-2000; 2000US-0256119P.
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05-DEC-2000; 2000US-0251030P.
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05-DEC-2000; 2000US-0251479P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
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08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
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17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
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ilarity 32.9%;
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Best Local Similarity
Matches 28; Conserv
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17-NOV-2000;
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01-DEC-2000;
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immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; gene therapy; channel/transporter protein; rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia; angiogenesis; nervous system disorder; Alzheimer's disease; coular disorder; corneal infection; wound healing; epithelial cell proliferation; skin aging; sunburn; transplantation; chemotaxis; food additive.
                                                                                                                                       Protein encoded by novel human channel/transporter gene #120 clone 2
77 TCPNXLDLPXYXSXXXXXXXXXXX 101
             481 TCFNRIDIPPYESYEKLYEKLLTAI
                                                                        ADM20055 standard; protein; 514 AA
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2000US-0224519P.
2000US-0225213P.
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2000US-0220963P.
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08-NOV-2000;
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25-SEP-2000;
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26-SEP-2000;
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17-NOV-2000; 2
01-DEC-2000; 2
05-DEC-2000; 2
              17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Rosen CA, Barash SC,

WPI; 2001-476159/51. N-PSDB; ADM19576. Isolated nucleic acid molecule encoding a channel/transporter protein is used in preventing, treating or ameliorating a medical condition.

Claim 11; SEQ ID NO 862; 809pp; English.

The invention relates to an isolated nucleic acid molecule encoding a channel/transporter protein or sequences at least 95% identical to a channel/transporter protein or sequences at least 95% identical to a chase. The nucleic acids and proteins encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to dispensing a parhological condition or susceptibility to a susceptibility to a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. concentration and social arthritis, cardiovascular disorders e.g. cardiovascular disorders e.g. cerbral isohemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by acteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease constructions.

Sequence 514 AA;

ò 46.9%; Score 127; DB 4; Length 514; llarity 32.9%; Pred. No. 7.8e-15; Conservative 3; Mismatches 54; Indels Best Local Similarity Matches 28, Conserv Query Match

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101 TCFNXLDLPXYXSXXXXXXXXXXXI ----------77

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2000US-0229343P

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2000US-0231244P

2000US-0231249P

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2000US-023239P
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22-AUG-2000;
33-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
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17-NOV-2000;
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13-OCT-2000;
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    meuroprotective; nootropic; antiparkinsonian; anticonvulsant;

antidiabetic; antirheumatic; antiarthritic; dermatological;

antidiflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;

anti-HIV; hepatotropic; virucide; antibacterial; fungicide;

antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;

cardiovascular; antiarteriosclerotic; antiarthythmic; cardiant;

Mrabimer's disease; Parkinson's disease; Huntington's chorea;

amyotrophic lateral sclerosis; multiple sclerosis;

immune system disorder; disbetes; rheumatoid arthritis;

systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;

inflammatory disorder; ischaemia-reperfusion injury;

inflammatory disorder; ischaemia-reperfusion injury;

inflammatory bowel disease; Crohn's disease; inflection;

fungal infection; parasitic infection; muscular disorder;

reproductive disorder; gastrointestinal disorder;

renal disorder; acute glomerulonephitis; pyelonephritis;

renal disorder; acute glomerulonephritis; pyelonephritis;

renal lithiasis; proliferative disorder; cancerous diseases; human.
  481 TCFNRIDIPPYESYEKLYEKLLTAI 505
                                                                                                 ADI54616 standard; protein; 514 AA
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24-FEB-2000; 2000US-0186464P.

22-FEB-2000; 2000US-0186450P.

25-FEB-2000; 2000US-0186450P.

16-MAR-2000; 2000US-0189874P.

17-MAR-2000; 2000US-0199174P.

18-AFR-2000; 2000US-0199174P.

19-MAY-2000; 2000US-01298174P.

28-JUN-2000; 2000US-0216647P.

20-JUN-2000; 2000US-0216647P.

20-JUL-2000; 2000US-021664P.

11-JUL-2000; 2000US-021664P.

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14-JUL-2000; 2000US-021664P.

14-JUL-2000; 2000US-021664P.

14-JUC-2000; 2000US-02161BP.

14-JUC-2000; 2000US-022651BP.

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14-JUC-2000; 2000US-022521BP.

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14-JUC-2000; 2000US-0225266P.

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14-JUC-2000; 2000US-0225267P.

14-JUC-2000; 2000US-0225267P.

14-JUC-2000; 2000US-0225267P.
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2000US-0225758P.
2000US-0225759P.
2000US-0226279P.
2000US-022681P.
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Protein ubiquitin ligase; publ; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.
                                                                                                          Human protein ubiquitin ligase publ.
                             AAW13384 standard; protein; 748 AA.
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                                                                                                                                                                              Homo sapiens.
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AAW13384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence at least 90% identical to: a polypeptide fragment, domain, espitope, or full-length protein of any one of 607 amino acid sequences (I) described in the specification; a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions which a neural disorders, e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis, immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions e.g. neural disorders, reproductive disorders or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated polypeptide comprising an amino acid
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46.9%; Score 127; DB 8;
Best Local Similarity 32.9%; Pred. No. 7.8e-15;
Matches 28; Conservative 3; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC;
         17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-025198P.
0S-DEC-2000; 2000US-025198P.
0S-DEC-2000; 2000US-025198P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
0S-DEC-2000; 2000US-025186P.
                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
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N-PSDB; ADI54018.
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RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (RUBE/) F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases
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96WO-US015930. 95US-00539205.

(first entry)

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Human protein ubiquitin ligases publ (AAW13381), pub2 (AAW13385) and pub3 (AAW13386) are homologues of fission yeast publ (AAW13387) and were identified from cDNA clones (AAT47040-42) obtd. e.g. from a keratinocyte CDNA library. Pub polypeptides can be produced in transfected host cells. They can control the steady state level of cd25 phosphatese, the degree of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of p53). They can regulate cell or tissue differentiation, or cell growth or proliferation by affecting other proteins, can be a specific (ant)agonist of wild type protein function and may be used as immunogens to elicit a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a human Smurf2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.9%; Score 127; DB 2; 32.9%; Pred. No. 1.1e-14; tive 3; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 TCFNXLDLPXYXSXXXXXXXXX 101
                                                                                                                                                                                                                                                Claim 1; Page 74-77; 108pp; English.
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Caligiuri M,
                                                        WPI; 1997-226206/20.
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                                                                                 N-PSDB; AAT47040.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune residue
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Best Local Simi:
Matches 28;
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  Beach D,
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ID AAB3
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0; Gaps

54; Indels

421 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 480

TCFNXLDLPXYXSXXXXXXXXXX 101 481 TCFNRIDIPPYESYEKLYEKLLTAI 505

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17 WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXX 76

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFWKAVEFFDEERRARLLOFVTGSSRVPLOGFKALOGAAGPRLFTIHOIDACTNNLPKAH 714
Smurf1; Smurf2; Smad signal transduction; bone morphogenic protein; BMP; transforming growth factor-beta; human; TGF-beta; chondrogenesis; lood differentiation; cartilage formation; hair growth; neural tube patterning; retinal development; heart induction; morphogenesis; tooth formation; gamete formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 WFWXIXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXLPXXH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated Smurf protein useful for inhibiting bone morphogenic protein or tumor growth factor-beta activation pathway, for treating cancer and to block osteogenesis, hair growth, tooth formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth; differentiation; blood endothelial cell; BEC;
lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 127; DB 4; Length 748; 32.9%; Pred. No. 1.1e-14; ive 3; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BEC/LEC-related protein sequence SeqID674.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Fig 12; 107pp; English.
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                                                                                                                                                                                                                                                           99US-0138969P
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les 28; Conservative
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                                                                                                                                                                                                                                                           11-JUN-1999;
                                                                                                                Homo sapiens
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic condothelial cells with a composition comprisition an agent that differential cells with a composition comprisition an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGRA-; and administering to the subject a composition composition composition and plymucleorides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, the development of compounds with an antiangiogenic, cytostatic, composition antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cells disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cells. The agent is useful in manufacturing a cell or lymphatic prowth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a control of other diseases involving the lymphatic system. The present sequence is that of a human LEC/BEC differentially control and a control of the method of the invention. We have not the method of the invention when the control and a control and a control of the method of the district of the method of the method of the district of the method of the district of the method 
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vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
inflammatory disease; cancer metastasis; lymphatic system; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 674; 176pp; English
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                                                                                                                                                                                                         07-MAR-2003; 2003WO-US006900.
                                                                                                                                                                                                                                                       07-MAR-2002; 2002US-0363019P.
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                                                                                                                                                                                                                                                                                                                        (LICN ) LICENTIA LTD
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nes 28; Conserv
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                                                                                                              WO2003080640-A1
                                                                   Homo sapiens.
                                                                                                                                                            02-OCT-2003
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c expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (1) and (II) may be used to treat disease, for example, cell proliferative disorder, crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in camples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAU19415-AAU19625 represent human diagnostic and therapeutic (DITHP) polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       711 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 127; DB 4; 32.9%; Pred. No. 1.2e-14; tive 3; Mismatches 54;
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Best Local Similarity 32.99
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 804 AA;
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ADN05464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DTTHP) polypeptides (II), which include e.g. enzymes, and proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosm data treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC; D'sa SA, Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour GE; Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF; AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A; Ya PE, Yu JY, Bradley DL, Bracher SR, Chen W; Hodgson DM, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics.
                                                                                             Human, receptor, diagnostic; therapeutic; gene therapy, vaccine;
cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;
acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                  Human diagnostic and therapeutic polypeptide (DITHP) #196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 512-514; 522pp; English.
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2000US-0184772P.
2000US-0184773P.
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2000US-0184776P.
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2000US-0185213P.
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       (first entry)
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Cohen HJ, Hodgson DM,
                                                                                                                                                                  respiratory disorder.
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24-FEB-2000;
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24-FEB-2000;
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24-FEB-2000;
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12-MAY-2000;
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24-FEB-2000;
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Flores V,
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Length 804; 54; Indels 9

Wood WI;

Schoenfeld J, Williams PM,

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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then by selecting a bait protein from a known adipocyte are identified by selecting a bait protein show is a performing a past 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a recombinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 anion acid cells, a SID (RTM) polypeptide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polypeptides and a reconficating all or part of the data, listed in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                               WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 797
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                                                                                                                                                                                                                                                                                                                                 WFWXIXXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXLPXXH
                                                                                                                                                                                                                                                                       Gaps
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above sequences. The nucleic acid is useful for preparing a comfor diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
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                                                                                                                                                                                                      Length 831;
                                                                                                                                                                                                                                                                    54; Indels
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                                                                                                                                                                                               Score 127; DB 8;
Pred. No. 1.3e-14;
3; Mismatches 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCFNXLDLPXYXSXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822
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TCFNRIDIPPYESYEKLYEKLLTAI
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32.9%;
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                                                                                                                                                                                                                                                                    28; Conservative
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                                                                                                                                  Sequence 831 AA;
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                                                                                                                                                                           Query Mac.
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The complex, polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obssity or diabetes. The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening drugs that modulare the protein interaction, thus exhibiting the therapeutic effect. The present sequence represents a SID
                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; PRO; immune related disease; inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritic; antiasthmatic; antidiabetic; antiinflammatory; antipsoritatic; antirhyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or
                                                                                                                                                                                                                                                          17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGPXXLXXXXXXXXXXXXXXXXXXLPXXH
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                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                                      55; Indels
                                                                                                                                                                                 Score 125; DB 6;
Pred. No. 5.4e-15;
2; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO protein sequence SEQ ID NO:705.
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                                                                                                              (prey) protein of the invention
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                                                                                                                                                                                     46.1%;
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                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                 Sequence 156 AA;
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N-PSDB; AAT62067
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antagonist of the polypeptide or an antibody that binds to the comprising a combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of diagnosing an immune related disease or an inflammatory immune response in mammal; (12) a method of identifying a compound that inhibits or minics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The PRO sequences have antiallergic, antianaemic, antiathricic, antiallergic, antiinflammatory, antipporiatic, antithyroad, CNS, dermatological, gastrointestinal, nemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular, nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid virucide activities, and can be used in gene therapy. The nucleic acid useful in diagnosing and treading an immune related disease and in stimulating an immune response. The present sequence represents a human processing an immune related disease and in
                                                                                                                                                                                                                                                                                                                                                                               17 WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXX 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                            46.1%; Score 125; DB 8; Length 308
32.9%; Pred. No. 1.1e-14;
ive 2; Mismatches 55; Indels
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.9
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                   Sequence 308 AA;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or alleifuc variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell camporate is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially cappound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound useful in treating pain and a pharmaceutical composition of small molecule that regulates the activity of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more oplypeptides or their antibodies. The polynucleotide or the compound that (e.g. spinal segmental nerve injury (Ghung), chronic constitiction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from wipo at the way obtained in electronic form directly from wipo at the print of the printed spared method in electronic form directly from wipo at the printed spared.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.1%; Score 125; DB 7; Length 310; 32.9%; Pred. No. 1.1e-14; ive 2; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW13387 standard; protein; 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US015930.
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Best Local Similarity 32.5.
Best Local Similarity
Local 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-226206/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 310 AA;
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antilnflammatory; cerebroprotective; antilipaemic; antidiabetic; immunosuppressive; neuroprotective; notropic; neurodeptic; tranquilizer; osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic; virucide; haemostatic; anti-HIV; antithyroid; thyromimetic; dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant; thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer; epene therapy; protein replacement therapy; human.
                                                                                                                              that affects cell cycle progression. Its amino acid sequence was deduced from a cDNA clone (AAT62067) isolated from a Schizosaccharomyces pombe CDNA library. Disruption of publ elevates the level of cdc25 protein in vivo increasing the activity of the tyrosine kinases, weel and miki, required to arrest cell cycle. Loss of weel function in a S. pombe cell carrying a disruption in the publ gene results in a lethal premature entry into mitosis; such lethal phenotype can be rescued by the loss of cdc25 function. Human homologues (see also AAW13384-86) of fission yeast publ have been identified
               Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and
                                                                                                                Fission yeast protein ubiquitin ligase publ (AAW13385) is a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic and therapeutic polynucleotide; dithp; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                 etzen D, Chinn J, Dufour GE, Jackson JL;
PB, Amehey SR, Dam TC, Liu TF, Gerstin EH;
Chen A, Marwaha R, Lan RY, Urashka ME;
Panesar IS;
                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID No 285.
                                                                                                                                                                                                                                                                                                                                    Length 804;
                                                                                                                                                                                                                                                                                                                                 Score 125; DB 2; Length 80.
Pred. No. 2.9e-14;
2; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCFNXLDLPXYXSXXXXXXXXXX 101
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                                                                               Claim 1; Page 94-98; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE31153 standard; protein; 2044 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 TCFNQLDLPAYESFEKLRHMLLLAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2002; 2002US-0349384P.
17-JAN-2002; 2002US-0349413P.
17-JAN-2002; 2002US-0349946P.
                                                                                                                                                                                                                                                                                                                                   46.1%;
32.9%;
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A Yap PE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-636732/60.
N-PSDB; ADE31342.
                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                    Sequence 804 AA;
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                                                proliferation.
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Peralta CH,
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                    Matches
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The invention relates to a novel isolated human diagnostic and the invention relates to a novel isolated human diagnostic and the cherepetic polymucleotide (designated dithp). The novel dithp polymucleotide sequences rousisting of base pairs fully defined in the specification; a polymucleotide comprissing a naturally occurring polymucleotide a polymucleotide complementary to identical to the dithp polymucleotide; a polymucleotide complementary to identical, or an RNA equivalent of any of the polymucleotide management of any of the polymucleotide members of antiaherity incleotide or its polymucleotide members of antiaherity incleotide members of antiaherity incleotide or its polymucleotide members of antiaherity incleotide or its polymucleotide members of antiaherity incleotide or its polymucleotide members of antiaherity incleotide or incleotide members of antiaherity, antithyvoid, thyrominetic, antiaherity antiaherity incleotide hemostatic, antiherimatic, anticomulant, thromopolytic, anticoagulant, anorectic, vacotropic, and antiaher of protein replacement therapy. The dithp polymucleotides or DTHHP polymucleotides polymethic can be used in gene therapy and protein replacement therapy. The dithp polymucleotides or DTHHP polymucleotides are useful for diagnosing, preventing or treating diseases diseases include cancers (e.g. adenocarcinoma, leukaemia, melanoma, brain cancer, breast cancer, cervix cancer, bone cancer, liver cancer, lung cancer, breast cancer, cervix cancer, bone cancer, liver cancer, lung attentions or theropolytic and synchimic polymure/inflammatory disorders (e.g. Athroiditis, Crohn's disease, Graves, disease, thyroiditis, multiple sclerosis, osteoarthritis, relations (e.g. viral, bacterial, fungal or parasitic infection), developmental disorders (e.g. thyroiditis, multiple sclerosis, osteoarthritis, scleroderma, systemic lupus erythematosus), infections (e.g. thyroiditis, multiple sclerosis, disorders (e.g. thyroiditis, multiple sclerosis, disorders (e.g. thyroiditis, multiple sclerosis, diso
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                                                 useful for diagnosing, treating or preventing e.g. leukemia, brain
cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
                       New human diagnostic and therapeutic polynucleotides and polypeptides, useful for diagnosing, treating or preventing e.g. leukemia, brain
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                                                                                                                                               Claim 27; SEQ ID NO 285; 634pp; English
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nes 28; Conservative
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                                                                                                   or Alzheimer's.
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Matches
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Search completed: October 13, 2005, 15:00:29 Job time: 252.297 secs

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MOLECULE TYPE: protein
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CITY: Boston
STATE: MA
TOPOLOGY:
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Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 31689, A
Sequence 46906, A
Sequence 46906, A
Sequence 45284, A
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Sequence 1, Appli
Sequence 1, Appli
                                                                                                     October 13, 2005, 13:50:53; Search time 51.4286 Seconds (without alignments) 156.763 Million cell updates/sec
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                                                                                                                                                                                   Description
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Sequence 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-270-767-48742
US-09-270-767-32280
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                                                                                                                                                                                                                                                                               513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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123.5
121
121
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No.
                                                                                                        Run on:
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642 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 701
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5, Appli
115, App
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124, App
75, Appl
58636, A
116, App
74, Appl
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19428, A
70, Appl
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APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
APPLICANT: Nefsky, Bradley
TILLE OF INVENTION: Ubjquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: One Post Office Square
                                                                                                                 Sequence Seq
Sequence Sequence Sequence
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46.9%; Score 127; DB 3; Length 735;
Best Local Similarity 32.9%; Pred. No. 4.7e-16;
Matches 28; Conservative 3; Mismatches 54; Indels
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                        US-08-630-916A-84
US-09-248-796A-19428
US-09-919-47-70
US-08-630-916A-79
US-08-630-916A-75
US-09-270-767-58636
US-09-270-767-58636
US-09-916A-116
US-09-916A-116
US-09-916A-115
US-09-916A-115
US-08-919-016-11491
US-08-919-016-11491
US-08-919-016-115
US-08-630-916A-15
US-08-630-916A-16
US-08-630-916A-16
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REGISTRATION UNMBER: 36,709
REFERRICE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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Patent No. 6001619
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Caligiuri, Maureen
APPLICANT: Wignitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

46.9%; Score 127; DB 4; Length 735;
Best Local Similarity 32.9%; Pred. No. 4.7e-16;
Matches 28; Conservative 3; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              702 TCFNRIDIPPYESYEKLYEKLLTAI 726
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
                                                                                                                      RESULT 2
18-08-392-163A-2
18-08-392-163A-2
18-90 No. 6503742
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
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STATE: MA
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US-08-539-205A-4
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Patent No. 6503742

GENERAL INFORMATION:

APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley

ITILE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.6%; Score 123.5; DB 3; Length 766; 34.1%; Pred. No. 2.3e-15; tive 3; Mismatches 52; Indels 1
                                                               MELLUM IIEEE TADAPY VALEN.

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELEPHONE: (617) 832-1000
TELEPAS: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFENCE/DOCKET NUMBER: CSV-005.01
TELECOMMINICATION: INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       733 TCFNRLDLPPYTSKKDLDHKLSIAV 757
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COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               : 766 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.19
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
                                                                                                                                                                                                            RESULT 7
US-08-630-916A-48
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                                                                                                                                                                                                                                             Sequence 31689, Application US/09270767

Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICANTON NUMBER: US/09/270,767
CURRENT APPLICANTON NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 31689
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 WFWXIXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXLPXXH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: F1806-03-4
CURRENT APPLICATION NUMBER: 15/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46906
LENGTH: 119
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                                                                                                                                                                       DB 4; Length 766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 119;
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                                                                                                                                                                                                            52; Indels
                                                                                                                                                                     Query Match 45.6%; Score 123.5; DB 4 Best Local Similarity 34.1%; Pred. No. 2.3e-15; Matches 29; Conservative 3; Mismatches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
15-09-270-767-46906
1 Sequence 46906, Application US/09270767
1 Patent No. 6703491
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US-09-270-767-46906
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ORGANISM: Drosophila melanogaster
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                                                       i LENGTH: 766 amino acids
i TYPE: amino acid
TOPOLOGY: linear
i MOLECULE TYPE: protein
US-09-392-163A-4
TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-09-270-767-31689
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Sequence 48, Application US/08630916A

Batent No. 601137

GENERAL INFORMATION:
APPLICANT: Firozzi, Gregorio
APPLICANT: Fay, Brian K.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   814 WFWQVVKEMDNEKRIRLLQFVTGTCRLPVGGFAELIGSNGPQKFCI-DKVGKETWLPRSH 872
                                                9/
                                                                              25 WFWRALRSFDQADRAKFLQFVTGTSKVPLQGFGSLEGMNGIQKFQIHRDDRSTDRLPCAH 84
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                                                17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXLPXXH
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  Gaps
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Pred. No. 1.1e-14;
1; Mismatches 52; Indels 1;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: New TOLK
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READBLE FORM:
COMPUTER: READBLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIONS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING BATE: 03.3-APR-1996
CLASSIFICATION: 435
  55;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LEGLIE
REGISTRATION NUMBER: 18,872
REFERRNCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPRNE: (212) 790-990
TELEPRX: (212) 896-8964/9741
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                        85 TCFNQLDLPMYKSYDKLRSCLLKAI 109
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Sequence 45284, Application US/09270767

SPACENT NO. 6703491

SPENERAL INFORMATION:

APPLICANT: Homburger et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 36.5%;
Matches 31; Conservative
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GENERAL INCORNATION:
APPLICANT: Kaser, Matthew R.
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NO 235
LENGTH: 752
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (136)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (428)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (198)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (235)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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CURRENT FILING DATE: 2001-07-09
FIROR PEDICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PatentIn Ver. 2.0
EAG ID NO 371
LENGTH: 474
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.0%; Score 116.5; DB 4; Length 474; Best Local Similarity 37.6%; Pred. No. 3.1e-14; Matches 32; Conservative 0; Mismatches 52; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 116.5; DB 4; Length 752;
Pred. No. 5.2e-14;
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OTHER INFORMATION: Incyte ID No. 6727066 1989186CDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 TČFNRLDLPPÝKSYEQLKEKLLFÄL 465
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; Sequence 235, Application US/09919039
; Patent No. 6727066
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36.5%;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                             FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) LOCATION: (23), (25)
, OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-18187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 WFWQVVESYSSEMRARLLQFVTGSSRVPLQGFRALQGSTGAVGPRLFTIHLTADVPTQNL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXLPXXH
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43.0%; Score 116.5; DB 4; Length 464;
Best Local Similarity 31.8%; Pred. No. 3.1e-14;
Matches 27; Conservative 3; Mismatches 54; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                     Score 119; DB 4; Length 384;
Pred. No. 8.2e-15;
6; Mismatches 53; Indels
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Patent No. 6806351
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PXXHTCFNXLDLPXYXSXXXXXXXXXX 101
                   FILE REFERENCE: File Reference: 7326-094
CURRENT PEPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45284
LENGTH: 384
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US-09-248-786A-18187
; Sequence 18187, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 29.2%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Candida albicans
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US-09-774-639-371
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                                                                                                                                                                                                                                                            SEQ ID NO 3
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                                                                    660 WFWQFVKEIDNEKRMRLLQFVTGTCRLPVGGFADLMGSNGPQKFCI-EKVGKENWLPRSH 718
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                                     17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXXX 76
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    1; Gaps
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Pred. No. 6e-14;
0; Mismatches 53; Indels 1
  53; Indels
                                                                                                                                                                                                                                                                                                                APPLICANT: Hustad, Carolyn M.
APPLICANT: Ghildyal, Mamit
TITLE OF INVENTION: Human E3 Ubiquitin Protein
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 11
ADDRESSPONDENCE ADDRESS:
ADDRESSEE: ZENECA Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,060
FILING DATE: 30-APR-1998
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: ZENECA Pharmaceuticals, Inc. STREET: 1800 Concord Pike CITY: Wilmington
                                                                                                                 77 TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                                                                         719 TCFNRLDLPPYKSYEQLKEKLLFAI 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 TCFNXLDLPXYXSXXXXXXXXXX 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/073,839
FILING DATE: 05-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
US-09-357-746-3
; Sequence 3, Application US/09357746
                                                                                                                                                                                                                                                        Sequence 3, Application US/09070060
Patent No. 5976849
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Higgins, Patrick H
REGISTRATION NUMBER: 39,709
REFERENCE/DOCKET NUMBER: PHH
TELECOMMINICATION:
TELEPHONE: 302.886.4889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19850-5437
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.0%;
36.5%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 852 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 36.5°
***ches 31; Conservative
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 302.886.8221
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D
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US-09-070-060-3
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760 WFWQFVKEIDNEKRMRLLQFVTGTCRLPVGGFADLMGSNGPQKFCI-EKVGKENWLPRSH 818
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                                                                                     TITLE OF INTERNICE: HUMAN E3 UBIQUITIN PROTEIN LIGASE FILE REFERENCE: PHM. 70312.N1
CURRENT APPLICATION NUMBER: US/09/357,746
CURRENT FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: US NO. 6087122 60/073,839
EARLIER PILING DATE: 1998-02-05
EARLIER PELING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRAUSEQ for Windows Version 3.0
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Sequence 4, Application US/09070060

Sequence 4, Application US/09070060

Patent No. 5976849

GENERAL INFORMATION:

APPLICANT: Hustad, Carolyn M.

APPLICANT: Ghildyal, Namit

TITLE OF INVENTION: Human E3 Ubiquitin Protein

TITLE OF INVENTION: Ligase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: ZENECA Pharmaceuticals, Inc.

STREET: 1800 Concord Pike
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MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETE COPENATION COMPATION COMPATION DATA: APPLICATION NUMBER: US/09/070,060 FILING DATE: 30-APR-1998 CLASSIFICATION NUMBER: 60/073,839 FILING DATE: TOORNEY, APPLICATION NUMBER: 60/073,839 FILING DATE: NAME: H3ggins, Patrick H3gg
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amino acid
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LENGTH: 854 amino acid
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GENERAL INFORMATION:
APPLICANT: ZENECA Limited
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ORGANISM: Homo sapiens
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762 WFWQFVKEIDNEKRMRLLQFVTGTCRLPVGGFADLMGSNGPQKFCI-EKVGKENWLPRSH 820
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                                                                                                                      Query Match 43.0%; Score 116.5; DB 2; Length 854; Best Local Similarity 36.5%; Pred. No. 6e-14; Matches 31; Conservative 0; Mismatches 53; Indels 1;
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GENERAL INFORMATION:
APPLICANT: ZEMECA Limited
TILLE OF INVENTION: HUMAN B3 UBIQUITIN PROTEIN LIGASE
FILE REFERENCE: PHM. 70312.N1
CURRENT APPLICATION NUMBER: US/09/357,746
CURRENT FILING DATE: 1990-07-21
EARLIER APPLICATION NUMBER: US NO. 6087122 60/073,839
EARLIER FILING DATE: 1998-04-30
SEARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
LENGTH: 854
                                                                                                                                                                                                                                                                                                                                            821 TCFNRLDLPPYKSYEQLKEKLLFAI 845
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STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
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CORGANISM: Mus musculus
US-09-357-746-4
                                                       , MOLECULE T)
US-09-070-060-4
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Search completed: October 13, 2005, 14:03:04 Job time : 52.5536 secs

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Sequence 3 Sequence 3

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Sequence

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Sequence Sequence Sequence Sequence

5703, Ap 14, Appl 14, Appl 10152, A 114, App 2, Appli

Sequence Sequence Sequence

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264 WFWEIVEEFDKEERAKLLÕFVTGSPRLPLQGFKSLEGSNGIPKFTIEKAGTEDERLPTAH 323
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Sequence 5, Application US/10268036

Sequence 5, Application US/10268036

Publication No. US20030100020A1

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: PAMILY MEMBER AND USES THEREFOR
FILE REFERENCE: MPOI-224PLRM
CURRENT APPLICATION NUMBER: US/10/268,036

CURRENT APPLICATION NUMBER: US 60/3210-09

PRIOR APPLICATION NUMBER: US 60/327,820

PRIOR PILING DATE: 2001-10-09

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 358
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US-10-313-955-2

US-10-756-149-4725

US-10-756-149-4725

US-10-220-120-407

US-10-043-487-200

US-10-043-487-200

US-10-043-487-285

US-10-043-487-285

US-10-047-143-17961

US-10-097-534-12

US-10-097-534-12

US-10-097-534-12

US-10-097-534-12

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US-10-097-534-10

US-10-097-534-10

US-10-374-979-89

US-10-38-38-468

US-10-477-133-668

US-10-38-3-28-7-296

US-10-287-218-3
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ORGANISM: Artificial Sequence
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Sequence 250383,
Sequence 250386,
Sequence 196183,
Sequence 196183,
Sequence 119793,
Sequence 119793,
Sequence 119793,
Sequence 11, Appli
Sequence 11, Appli
                                                                                                                                                                           October 13, 2005, 13:59:34; Search time 230.242 Seconds (without alignments) 195.471 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                Published Applications AA:*

1: \cgn2 \( \) \cgn \(\) \cgn \( \) \
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                           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-391-364-33
US-10-425-115-250383
US-10-425-115-29229
US-10-424-599-196163
US-10-424-599-196003
US-10-424-599-146004
US-10-307-956-1
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thoma K.
APPLICANT: Avoid K.
APPLICANT: Avoid K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 259386
                      TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REPERBNCE: 38-21 (3322) B
CURRENT APPLICATION NUMBER: US)10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 250383
LENGTH: 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
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                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: MRT4577_159941C.1.pep
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US-10-425-115-250386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.9%; Score 138; DB 16; Best Local Similarity 33.7%; Pred. No. 3.9e-17; Matches 31; Conservative 2; Mismatches 59;
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1111)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 292299, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-10-425-115-292299
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                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                              APPLICANY: MAYER, RAILEMAN PINAMEDEULICALS, INC.
APPLICANY: Carroll, Joseph M.
APPLICANY: Carcoll, Joseph M.
APPLICANY: Carcoll, Joseph M.
APPLICANY: Weich, Nadine S.
APPLICANY: WorkING NOWE 2003
TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND FILE REPRENCE: MPIO3-010-000-18
TILE REFERENCE: MPIO3-010-000-18
FILE REPRENCE: MPIO3-010-000-19
FRIOR FILING DATE: 2001-01-19
FRIOR FILING DATE: 2001-01-10
FRIOR FILING DATE: 2001-11-13
FRIOR FILING DATE: 2001-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 WFWXIXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXDXXH 76
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51.7%; Score 140; DB 16;
Best Local Similarity 37.6%; Pred. No. 1.9e-17;
Matches 32; Conservative 0; Mismatches 53;
                                                                                                                                                                     Sequence 33, Application US/10391364
Publication No. US20040121349A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
324 TCFNRLDLPKYSSKEILRSKLLLAI 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCFNRLDLPKYSSKEILRSKLLLAI 348
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APPLICANT: La Rosa, Thomas J.; APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COTHER INFORMATION: Consensus sequence US-10-391-364-33
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US-10-425-115-250383
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Sequence 146002, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53.22)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 292299
LENGTH: 61
TYPE: ...
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Squence 196163, Application US/10424599

Squence 196163, Application US/2A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (5223.3) B

CURRENT APPLICATION NUMBER: US/10/424, $99

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 196163

LENGTH: 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
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US-10-424-599-196163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_29661C.1.pep
US-10-425-115-292299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(661)
OTHER INFORMATION: unsure at all Xaa locations
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 32.6
Matches 30; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: ungure
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Sequence 119793, Application US/10437963
; Sequence 119793, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Plang
; APPLICANT: Li, Plang
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119793
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Scoul Soviet K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 146002
LENGTH: 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102859C.1.pep
US-10-424-599-146002
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US-10-437-963-119793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

49.8%; Score 135; DB 15;
Best Local Similarity 32.6%; Pred. No. 4.9e-16;
Matches 30; Conservative 3; Mismatches 59;
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OTHER INFORMATION: unsure at all Xaa locations
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LOCATION: (2)...(4)
OTHER INFORMATION: Xaa = any amino acid; 0-1 residues may be missing
                                                                                                  LOCATION: (6)...(16)
OTHER INFORMATION: Xaa = any amino acid; 0-3 residues may be missing
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OTHER INFORMATION: Xaa = Leucine, Valine, Methionine, Alanine or OTHER INFORMATION: Isoleucine
                                                                                                                                                                                                                                                                                                         LOCATION: (22)...(22)
OTHER INFORMATION: Xaa = Valine, Isoleucine or Leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (40)...(40)

OTHER INFORMATION: Xaa = Threonine or Serine
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OTHER INFORMATION: Xaa = Lysine or Arginine
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OTHER INFORMATION: Xaa = Valine or Leucine FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (34)...(34)
OTHER INFORMATION: Xaa = Leucine or Valine
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OTHER INFORMATION: Xaa = any amino acid
FEATURE:
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LOCATION: (41)...(41)
OTHER INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa = any amino acid
FEATURE:
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OTHER INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa
FEATURE:
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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AME/KEY: VARIANT
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NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                      Sequence 146004, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
FAPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Anou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 146004
LENGTH: 1843
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Publication No. US20030119072A1

Generatin Propertion:

APPLICANT: Hockstra, Marl F.

APPLICANT: Morestra, Marl F.

APPLICANT: Marray, Brion

FILE REFERENCE: 860984433

CURRENT APPLICATION NUMBER: US/10/307,956

CURRENT FILING DATE: 2002-12-02

PRIOR FILING DATE: 1999-08-03

NUMBER OF SEQ ID NOS: 32

SOFTWARE: RestSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 108
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WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXX 76
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48.7%; Score 132; DB 15; Length 1.

Best Local Similarity 32.9%; Pred. No. 2.9e-15;

Matches 28; Conservative 4; Mismatches 53; Indels
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US-10-424-599-146004
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OTHER INFORMATION: Xaa = Tyrosine or Phenylalanine
                                                                                                                                          1111 | 1 | 1 | 3613 TCFNQLDLPEXSSKEQLEERLLLAIHEASEGF 3644
                                                                                                    77 TCFNXLDLPXYXSXXXXXXXXXXXXXXXX 108
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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US-10-424-599-146004
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US-10-307-956-1
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RESULT 12
US-10-313-955-2
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; OTHER INFORMATION: Xaa = any amino acid; 0-2 residues may be missing US-10-307-956-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 819, Application US/09764875 | Publication No. US20040018969A1 | GENERAL INFORMATION: | APPLICANT: Rosen et al. | TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies | FILE REFERENCE: PJZ02 | CURRENT APPLICATION NUMBER: US/09/764,875 | CURRENT FILING DATE: 2001-01-17 | Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1249 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 1240 | SEQ
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Pred. No. 7.3e-15;
3; Mismatches 54; Indels
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INFORMATION: Xaa = Leucine or Methionine
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100.0%; Pred. No. co.
0; Mismatches
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INFORMATION: Xaa = any amino acid
ON: (81)...(81)
INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa = any amino acid
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32.9%;
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Best Local Similarity 100.
Matches 85; Conservative
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Best Local Similarity 32.9
Matches 28; Conservative
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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CORGANISM: Homo sapiens
US-09-764-875-819
                                                                                                                                                                                                                                        NAME/KEY: VARIANT LOCATION: (88)...
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US-09-764-875-819
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Gaps

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                                                                                                                                                                                                                                                                                                                               Caligiuri, Maureen
Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNBER: US/10/313,955
FILING DATE: 05-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matchew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/392,163
PLING DATE: «Unknown»
APPLICATION NUMBER: US 08/539,205
FILING DATE: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                      77 TCFNXLDLPXYXSXXXXXXXXX 101
                                                                                                   77 TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 702 TCFNRIDIPPYESYEKLYEKLUTAI 726
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; Sequence 81, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORNATION:
; APPLICANT: Murray, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                Sequence 2, Application US/10313955
Publication No. US20030199036A1
GENERAL INFORMATION:
APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 832-10 TELEFAX: (617) 832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 735 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.9%;
Matches 28; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
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60/184,770; 60/184,774;
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CURRENT PILLING DATE: 2002-08-26

CURRENT PILLING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 0/184,777; 60/184,698; 60/184,770; 60/184,777; 60/184,773; 60/184,776; 60/184,777; 60/184,773; 60/184,776; 60/184,777; 60/184,773; 60/184,771; 60/184,773; 60/184,811; 60/184,811; 60/184,772; 60/184,772; 60/184,812; 60/204,812; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/204,261; 60/205,281; 60/205,281; 60/205,281; 60/205,281; 60/206,224; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-17; 2000-02-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17; 2000-05-17;
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; OTHER INFORMATĪON: Incyte ID No. US20040048253A1 LG:132147.3.orf3:2000FEB18
US-10-220-120-407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHEN, Wensheng
APPLICANT: COHEN, Howard J.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.9%; Score 127; DB 15; Length 804; Best Local Similarity 32.9%; Pred. No. 1.1e-14; Matches 28; Conservative 3; Mismatches 54; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 TCFNXLDLPXYXSXXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSEN, Bruce H.
RUSSO, Frank D.
STOCKDREHER, Theresa K.
                                                                                                                                                                             CHANG, Simon C. CHEN, Alice D. SA, Steven A. AMSHEX, Stefan DAHL, Christopher R. DAMELS, Susan E. DUFOUR, Gerard E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FONG, Willy T.
GREENAMALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
LIU, TOMMY F.
ROSEBERRY, Ann M.
              PANZER, Scott R.
SPIRO, Peter A.
BANVILLE, Steven C.
                                                                                                                SHAH, Purvi
CHALUP, Michael S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shawn R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WRIGHT, Rachel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vincent
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LORES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAFFO,
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US-10-756-149-4725

US-10-756-149-4725

US-10-756-149-4725

Sequence 4725, Application US/10756149

Publication No. US20050181375A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A212, Natasha

APPLICANT: A212, Natasha

APPLICANT: A212, Natasha

APPLICANT: A1bert

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER,
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

TITLE OF PREBLOCATION NUMBER: US/10/756,149

CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12

NUMBER OF SEQ ID NOS: 5818

SOFTWARE: Patentin version 3.2

SEQ ID NO 4725
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: BOS Blocechnology, Inc.
TITLE OF INVENTION: No. US20030152226A1e1 Methods of Diagnosis of Angiogenesis,
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Modulators
TITLE OF INVENTION: Modulators
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
TITLE OF INVENTION: DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US/99/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-08-11
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     655 WFWKAVEPFDEERRARLLÓFVÍGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXXXX776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXTPXXH 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.9%; Score 127; DB 14; Length 7. Best Local Similarity 32.9%; Pred. No. 1e-14; Matches 28; Conservative 3; Mismatches 54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 32.9
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-756-149-4725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 81
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-021-660-81
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Search completed: October 13, 2005, 14:49:58 Job time: 232.242 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model 1 OM protein

October 13, 2005, 14:36:01; Search time 45.0989 Seconds (without alignments) 230.414 Million cell updates/sec Run on:

US-09-385-918-1 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SH	Description	protein F14J16.10	ubiquitin-protein	related to TOM1 pr	probable ubiquitin	ubiquitin protein	DNA binding protei	probable ubiquitin	ubiquitin-protein	ubiquitin-protein	hypothetical prote	ubiquitin ligase N	ubiquitin-protein	ubiquitin-protein	hypothetical prote	probable ubiquitin	E6-associated prot	hypothetical prote	hypothetical prote	probable membrane	probable ubiquitin	hypothetical prote	polyubiquitin-like	hypothetical prote	probable ubiquitin	giant protein p619	probable ubiquitin		hypothetical prote	
SUMMAKIES	ID	H96599	T01491	T49799	T37964	T39585	I52646	T37900	S66562	T37545	S69625	S70642	843217	T46412	T51886	T49744	A38920	T20274	B38919	S57055	T40821	S30015	H85134	T47165	T38617	S71752	T38951	T20373	T21546	770700
	DB	5	~	7	7	~	7	7	-	7	~	~	Н	~	7	7	~						~	7	~	~	7	~	7	ç
	Query Match Length	4056	1126	3839	3227	786	310	671	99/	167	3268	887	809	820	221	815	874	889	1054	892	807	1483	873	52	632	4861	1029	1001	2899	2017
ď	Query	49.8	49.4	48.0	47.6	46.7	46.1	45.6	45.6	45.6	43.2	43.0	42.6	41.9	41.5	41.1	37.1	36.7	36.7	30.6	30.4	29.9	29.0	28.8	28.4	28.0	27.9	27.5	26.8	26 8
	Score	135	134	130	129	126.5	125	123.5	123.5	123.5	117	116.5	115.5	113.5	112.5	111.5	100.5	99.5	99.5	83	82.5	81	78.5	78	77	9/	75.5	74.5	72.5	7.0
	Result No.		8	m	4	Ŋ	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2
T01491
ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana
ubiquitin-protein ligase homolog F1707.15 - Arabidopsis thaliana
(c.Species: Arabidopsis thaliana (mouse-ear cress)
C.Bate: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004
C.Bate: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004
C.Bate: T01491
R;Vysotskaia, V.S.; Schwartz, Jr.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li,
R;Vysotskaia, V.S.; Schwartz, June 1998
A;Pescription: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.
A;Reference number: Z14334
A;Reference number: Z14334
A;Reference number: Z14334
A;Reference number: Z1434
A;Reference number: Z14334
A;Reference number: Z14334

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hypothetical prote	hyperplastic discs	hypothetical prote	hypothetical prote	hypothetical prote	NEDD-4 ORF - mouse	hypothetical prote	probable ubiquitin	herc2 protein - mo	hypothetical prote	protein F07G6.6 (i	chalcone synthase-				
T48309	T08437	S64155	A38919	T05688	183196	T26753	T46155	S22659	T29285	T14761	T41750	T14346	T06977	F89468	JC7639
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26	56	56	25	24	24	24	24	23	23	21.8	21	20	18	14	14
72	72	70.5	69.5	67	99	99	99	63	63	29	28	22	4	39	38
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1

H96599	
protein F14J16	protein F14J16.10 [imported] - Arabidopsis thaliana
C;Species: Aral	C;Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar	C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: H96599	196299
R, Theologis, A	R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W., C	Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; H	Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000	16-820, 2000
A; Authors: Hun	nter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.	C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Roo	oney, T.; Rowley, D.; Sakano, H.
A; Authors: Sal	A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D	ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A, Title: Seque	ence and analysis of chromosome 1 of the plant Arabidopsis.
A, Reference nu	A; Reference number: A86141; MUID: 21016719; PMID: 11130712
A; Accession: H96599	196599
A;Status: preliminary	liminary
A; Molecule type: DNA	DNA DNA
A; Residues: 1-4056 <sto></sto>	-4056 <sto></sto>
A; Cross-refere	A; Cross-references: UNIPROT: Q9LG27; GB: AE005173; NID: g8778329; PIDN: AAF79338.1; GSPDB: GN
C, Genetics:	
A,Gene: F14J16.10	5.10
A; Map position: 1	1: 1
Ouerv Match	49.8%; Score 135; DB 2; Length 4056;
Bear Local Similarity	37 68
Matches 30	36.05; ativo
	כסוופטו גמנוזגט ס' נודמוומרנוזנט ס' דוומניזט ס' סקדם
Qy 17	17 WFWXIXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXXX 76
3962 a	3962 WFWEVVKAFSKEDMARFLQFVTGTSKVPLBGFKALQGISGPQRLQIHKAYGAPERLPSAH 4021

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Length 3227;

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Score 129; DB 2;
Pred. No. 1.2e-15;
3; Mismatches 60
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32.9%;
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ilarity 31.5%;
Conservative 3
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Best Local Similarity 35.33
Matches 30; Conservative
                                                                                                            Query Match
Best Local Similarity
....hes 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: SPDB:SPBC16E9.11c
                                    A;Gene: SPDB:SPAC19D5.04
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
A;Introns: 60/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37964
E;Devlin, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
B;Devlin, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: Z21757
A;Reference number: Z21757
A;Accession: T37964
A;Accession: T37964
A;Accession: T37964
A;Accession: T37964
A;Residues: Jraliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3227 cDEV
C;Genetics:
A;Molecule type: DNA
A;Residues: 1-1126 <VYS>
A;Cross-references: UNIPROT:O64605; EMBL:AC003671; NID:g2833627; PID:g3176690; GSPDB:GNC
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternate names: protein [imported] - Neurospora crassa
N.Alternate names: protein B11B22.10
N.Alternate names: protein B11B22.10
N.Alternate names: protein B11B22.10
C.Species: Neurospora crassa
A.Reference number: Z2502
A.Residue: prediminary
A.Residue: prediminary
A.Residues: 1-3839 <-SCA-
A.Residues: 1-3839 <-SCA-
A.Residues: 1-3839 <-SCA-
A.Residues: 1-3819 <-SCA-
A.Resi
                                                                                                                                                                                                                    A;Gene: ATSP:F1707.15
A;Map position: 1
A;Introns: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
F;756-1120/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1032 WFWEVVKAFSKEDMARFLQFVTGTSKVPLEGFKALQGISGPQRLQIHKAYGSPERLPSAH 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXT76
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

49.4%; Score 134; DB 2;
Best Local Similarity 32.6%; Pred. No. 4.6e-17;
Matches 30; Conservative 3; Mismatches 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCFNQLDLPEYQSKEQVQERLLLAIHEANEGF 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: NCSP:B11B22.10
A;Map position: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3805
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-786 <000L>
A;Cross.references: UNIPROT:014326; EMBL:Z99759; PIDN:CAB16903.1; GSPDB:GN00067; SPDB:SPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA binding protein - rat
C;Species: Rattus sp. (rat)
C;Species: C.5Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: 152646
R;Gu, J.; Ren, K.; Dubner, R.; Iadarola, M.J.
Brain Res. Mol. Brain Res. 24, 77-88, 1994
A;Title: Cloning of a DNA binding protein that is a tyrosine kinase substrate and recogn
A;Reference number: 152646; MUID:95058008; PMID:7968380
                                                       3133 WFWRAVRSFDEEERAKLLQFATGTSKVPLNGFKELEGMSGFQRFNIHKSYGSLNRLPQSH 3192
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   9/
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                                                                                                                                                                                                                                                                                                                                                             ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)
US.Species: Schizosaccharomyces pombe
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39585
R;Volkaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: Z21865
A;Reference number: Z21865
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Amolecule type: mRNA
A;Residues: 1-310 <RES>
A;Cross-references: EMBL:U08214; NID:g475515; PIDN:AAA81950.1; PID:g475516
17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology $236-237.0main: WW repeat homology <WWR1> F;367-343/Domain: WW repeat homology <WWR2> F;364-401/Domain: WW repeat homology <WWR2> F;364-401/Domain: WW repeat homology <WWR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 125; DB 2; Length 310;
Pred. No. 6.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 8.6e-16;
2; Mismatches 52;
                                                                                                                                                                                  | | | | | | | | | :
TCFNQLDLPEYDTYEQLRSMLLTAINEGSEGF 3224
                                                                                                                                         A; Experimental source: strain 972h-; cosmid c16E9
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96

Matches

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ubiquitin-protein ligase (EC 6.3.2.19) publ [validated] - fission yeast (Schizosaccharom N;Alternate names: ubiquitin ligase Publ N;Alternate names: ubiquitin ligase Publ C;Decessors Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T37545; T48655 Stroken, D; Barrell, B.G.; Rajandream, M.A.; Wood, V. Submitted to the EMBL Data Library, September 1997 A;Reference number: Z21722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q92462; EMBL:Z99161; PIDN:CAB16207.1; GSPDB:GN00066; SPDB:SP
A;Experimental source: strain 972h-; cosmid c11G7
R;Saleki, R.; Jia, Z.; Karagiannis, J.; Young, P.G.
Mol. Gen. Genet. 254, 520-528, 1997
A;Title: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ ub A;Title: Tolerance. 207985; MUID:97340937; PMID:9197411
A;Accession: T48655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Punction: <CYC>
A;Description: involved in of the mitotic activating tyrosine phosphatase cdc25 (validat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 WFWELMDEWSNEKKSRLLLOFTTGTSRIPVNGFKDLQGSDGPRKFTI-EKAGEPNKLPKAH 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          675 WFWELMDEWSNEKKSRLLQFTTGTSRIPVNGFKDLQGSDGPRKFTI-EKAGEPNKLPKAH 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1.767 - 428
A.Cross-references: EMBL:U62795; NID:g2262192; PIDN:AAB63350.1; PID:g2262193
A.Experimental source: strain J227
                                                                                                                                                                                                                                                                                                                                                                                                    17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
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                                                                                                                                                                                                                                                                                                                     Gaps
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C, Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
C, Keywords: cell cycle control; ligase
F, 205-24/Domain: WW repeat homology < WW1>
F, 288-325/Domain: WW repeat homology < WW2>
F, 345-382/Domain: WW repeat homology < WW3>
                                                                                                                                                                                                                                                                                                                 7
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                                                                                                                                                                                                                    Length 766;
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                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                     52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: 1
A;Introns: 6/2; 14/1; 62/2
C;Function: cUB1>
A;Description: EC 6.3.2.19 [validated, MUID:96205868]
                                                                                                                                                                                                                             Score 123.5; DB 1
Pred. No. 3.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <MCL>
                                                                                                                                                                                                                                                                                                            3; Mismatches
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C; Keywords: ligase
F;205-242/Domain: WW repeat homology <WW1>
F;288-25/Domain: WW repeat homology <WW2>
F;345-382/Domain: WW repeat homology <WW3>
                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.1%;
Matches 29; Conservative
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Best Local Similarity 34.11
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T37545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Function: <TOL>
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NyAlternate names: E5-AP-like protein ubiquitin ligase
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S6562; T45159
EMBO J. 15. 1301-1312, 1302
EMBO J. 15. 1301-1312, 1302
A;Accession: S6552; MUID:96205868; PMID:8635463
A;Accession: S6552; MUID:96205868; PMID:8635463
A;Accession: S6552
A;Accession: Section Sequence not shown
A;Molecule type: mRNA
A;Accession: Tote Library, August 1996
A;Accession: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of A;Accession: T45159
A;Accession: Day
A;Molecule type: mRNA
A;Residues: 1-766
A;Bentics: Labininary; translated from GB/EMBL/DDBJ
A;Genetics:
C;Genetics:
A;Genetics:
A;G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Accession: T37900
R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: 221752
A;Accession: T37900
A;Reference number: 221752
A;Accession: T37900
A;Reference number: 221752
A;Accession: T37900
A;Reference number: 221752
A;Cession: T37900
A;Cession: T3790
A;Cession
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                                                                                                                                                   579 WFWELLSEWSPEKKAKLLQFATGTSRLPLSGFKDMHGSDGPRKFTI-EKVGHISQLPKAH 637
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                                                                                       17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXLPXXH
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         Gaps
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    55; Indels
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45.6%; Score 123.5; DB 2;
Best Local Similarity 34.1%; Pred. No. 2.8e-15;
Matches 29; Conservative 3; Mismatches 52;
2; Mismatches
                                                                                                                                                                                                                                                              77 TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                     274 TCFNQLDLPAYESFEKLRHMLLLAI 298
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28; Conservative
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A; Modecule type: DNA
A; Residues: 1-809 <DIE>
A; Cross-references: EMBL: U18916; NID: 91384128; PIDN: AAC03223.1; PID: 9603364; GSPDB: GN000
R; Hein, C.; Springael, J.Y.; Volland, C.; Haguenauer-Tsapis, R.; Andre, B.
Mol. Microbiol. 18, 77-87, 1995
A; Title: NEIL, an essential yeast gene involved in induced degradation of Gapl and Fur4 I
A; Reference number: $70050; MUID: 96154942; PMID: 8596462
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Ww repeat homology
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C.Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquit
C.Keywords: ligase
F;142-179/Domain: WW repeat homology «WWR1»
                                                                                                                                                                                                            A,Accession: S43217
A,Molecule type: DNA
A,Residues: 1-809 «MUL»
A,Cross.references: UNIPROT:P39940; GB:U18916; EMBL:L11119; NID:g1384128; PIDN:AAC03223.
                                                                                                                                                                                                                                                                                                                                    R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda
A;Reference number: S50628
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S43217; S50628; S70050
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      717 WFWKCVSEWDNEORARLLÖFTTGTSRIPVNGFKDLOGSDGPRRFTI-EKAGEVQQLPKSH 775
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C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquitin-protein ligase (EC 6.3.2.19) NEDD4 - human (fragment) N/Alternate names: hypothetical protein DKFZp434P2422.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Realdues: 1-820 < AAA>
A;Residues: 1-820 < AAA>
A;Cross-references: UNIPROT:Q9NT88; EMBL:AL137469
A;Experimental source: adult testis; clone DKFZp434P2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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31.8%; Pred. No. 1.1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: involved in endocytosis of GAP1 C, Superfamily: yeast ubiquitin-protein ligase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Gene: SGD:RSP5; PUB1; NP11; MIPS:YER125w
A.Cross-references: MIPS:YER125w; SGD:S0000927
A.Map position: 5R
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TCFNRVDLPQYVDYDSMKQKLTLAV 800
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F;331-368/Domain: WW repeat homology <WW2>
F;387-424/Domain: WW repeat homology <WW3>
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Best Local Similarity 31.8'
Matches 27; Conservative
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A; Residues: 1-101 <HEI>
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CjSpecies: Rattus norvegicus (Norway rat)
CjSpecies: Rattus norvegicus (Norway rat)
CjSpecies: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
CjAccession: 570642
EMBO J. 15, 2371-2380, 1996
A;Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+)
A;Reference number: 570642; MUID:96221297; PMID:8665844
A;Accession: 570642
A;Accession: 570642
A;Residue; preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-887 <STA>
A;Cross-references: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
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C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology «KC2»
F;54-167/Domain: www repeat homology «WW1»
F;246-283/Domain: www repeat homology «WW2»
F;402-439/Domain: www repeat homology «WW3»
F;459-496/Domain: www repeat homology «WW3»
F;555-881/Domain: ubiquitin-protein ligase homology «UBI»
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q03280; EMBL:U33050; NID:g927726; PIDN:AAB64910.1; PID:g927
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N;Alternate names: E6-AP-like protein ubiquitin ligase; protein YER125w; PUB1 protein
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                                                               Appothetical protein YDR457w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S69625
R;Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 5 A;Reference number: S69554
A;Moccession: S69625
A;Molecule type: DNA
A;Residues: 1-3268 <DIE>
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Pred. No. 7.8e-14;
2; Mismatches 53; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 117; DB 2; Length 3268;
Pred. No. 2.3e-13;
4; Mismatches 54; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: SGD:S0002865; MIPS:YDR457w
A;Map position: 4R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCFNXLDLPXYXSXXXXXXXXX 101
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31.8%;
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Best Local Similarity 34.1%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 31.8 ses 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SGD: TOM1
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R; Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A; Reference number: 225022
A; Accession: T49744
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-815 <SCH3
A; Residues: 1-815 <SCH3
A; Residues: 1-815 <SCH3
A; Residues: L1815 <SCH3
A; Residues: Usprelininary
A; Molecule type: DNA
A; Residues: L1815 <SCH3
A; Residues: L1815 <SCH3
A; Residues: L1815 <SCH3
A; Residues: L1815 <SCH3
A; Coss-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.160
A; Rap postion: 6
A; Introns: 11/1; 24/1; 59/2; 110/1; 783/2
C; Genetics:
A; Geneti
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Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
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Ciprocies: Homo sapiens (man)
Cipate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change
Cipatession: T51886
R;Blum, H: Bauersachs, S:; Mewes, H:W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25854
A;Reference number: Z25854
A;Accession: T51886
A;Accession: T51886
A;Accession: T51886
A;Accession: T51886
A;Accession: UNINA
A;Residus: Jrcaliminary
A;Molecule type: mRNA
A;Residus: J-221 cAAA>
A;Css-references: UNIRROT:09NPS9; EMBL;AL390186
A;Experimental source: adult testis; clone DKFZp434N1131
C;Genetics:
A;Note: DKFZp434N1131.1
                                                                                                                                                                           Query Match
41.9%; Score 113.5; DB 2; Length 8
Best Local Similarity 32.9%; Pred. No. 2.7e-13;
Matches 28; Conservative 3; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.5%; Score 112.5; DB 2; Length ilarity 31.8%; Pred. No. 1.1e-13; Conservative 3; Mismatches 54; Indels
F;342-379/Domain: WW repeat homology <WWR2>
F;393-430/Domain: WW repeat homology <WWR3>
F;489-814/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T51886
hypothetical protein DKFZp434N1131.1 - human (fragment)
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Search completed: October 13, 2005, 15:11:12 Job time: 47.0989 secs

Oracle Report of the State of t

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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October 13, 2005, 14:03:23 ; Search time 205.714 Seconds (without alignments) 268.842 Million cell updates/sec US-09-385-918-1 271 1 XXXXXXXXXXXXXXXXWFWX.....SXXXXXXXXLXXAIXXXXXXF 108 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

<u> </u>																						-								
Description		Q6K3Y/ Oryza Bariv O8hOt4 arabidonsis		Q9gup2 caenorhabdi	_			_	mus	Q8k300 mus musculu	Q80wx3 mus musculu	Q6p066 mus musculu	Q9cse3 mus musculu	Q96de7 homo sapien	Q9hau4 homo sapien	Q6cws8 kluyveromyc	O14326 schizosacch	Q9cu76 mus musculu	Q6axc1 mus musculu	P51593 rattus norv	Q7tmy8 mus musculu		Q756g2 ashbya goss		Q92462 schizosacch	Q7psq3 anopheles g			Q9vxr3 drosophila	Q9ct73 mus musculu
SUPPRETES	UPL1 ARATH	COKSI/	O6BJ34	Q9GUP2	TOM1_NEUCR	PTR1_SCHPO	Q6CFL1	QBNDDB	SUFI_MOUSE	Q8K300	QBOWX3	Q6P066	Q9CSE3	Q96DE7	SUF2 HUMAN	Q6CWS8	PUB3 SCHPO	Q9CU <u>7</u> 6	Q6AXC1	URB1_RAT	URB1_MOUSE	URB1_HUMAN			PUB1_SCHPO	Q7PSQ3	Q8T3L0	Q6FMP7	Q9VXR3	Q9CT73
h DB	4	ο α	9	7 2	r H	7	0	2	9	8	3	0	8	8	8	7	1 9	2	1	7	9	0	8		7	3	4	7 2	7	8
Lengt	3684	3658	334	4177	4065	3227	3320	295	619	728	13	19	258	28	748	324	78	159	321	322	2749	3360	325	671	767	983	964	3247	5146	108
% Query Match Length DB	8.6	4 4 0 4	48.7	48.3	48.0	47.6	47.6	47.2	47.2	47.2	46.9	46.9	46.9	46.9	46.9	46.9	46.7	46.1	46.1	46.1	46.1	46.1	45.8	45.6	45.6	45.4	44.6	44.6	44.6	44.5
Score	135	135	132	131	130	129	129	128	128	128	127	127	127	127	127	127	126.5	125	125	125	125	125	124	123.5	123.5	123	121	121	121	120.5
Result No.	<b>н</b> с	7 r	. 4	S	9	7	80	o,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

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WWP2_HUMAN WWP2_MOUSE 080YC4 080YC4 060Y1 06F901 08C5W5 015033 08CHG5 08BSC0 SUP1_KENLA SUP1_HUMAN 09V853	Q71MG3
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8470 8823 8823 8823 8826 8826 7311 7311 7410	252
# # # # # # # # # # # # # # # # # # #	43.7
120.5 120.5 120.5 120 120 120 119.5 119.5 119.5	118.5
и и и и и и и и и и и и и и и и и и и	<b>4</b>

# ALIGNMENTS

RESULT UPLI A: ID UPLI A: DT 2	LT 1 ARATH
1588 1588	25-OCT-2004 (Rel. 45, Last annotation update) E3 ubiquitin protein ligase UPL1 (EC 6.3.2) (Ubiquitin-protein ligase 1).
S G	Name=UPL1; OrderedLocusNames=At1g55860; ORFNames=F14J16.14, F14J16.37;
38	Ardbidopsis Luditana (Modec-ed Cress). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
88	Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsis.
N N	NCBI_TaxID=3702;
RP 0	SEQUENCE FROM N.A., PROBABLE FUNCTION, TISSUE SPECIFICITY,
22	STRAIN=cv. Columbia;
X X	MEDLINE=20040063; PUDMEQ=105/18/8; Bates P.W. Vierstra R.D.:
RT	"UPL1 and 2, two 405 kDa ubiquitin-protein ligases from Arabidopsis
R. T.	thaliana related to the HECT-domain protein tamily."; Plant J. 20:183-195(1999).
RN	[2]
я С	SEQUENCE FROM N.A.
X X	SIKAIN=CV. COLUMDIA; MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA 6	Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
<b>5 5</b>	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
\$ \$	A Dunn P., Ergu P., Feldbiyum T.V., Feng JD., Fong B., Fujil C.Y., A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA	Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
8 8	Kim C.J., Koo H.L., Kremenetskala I., Kurcz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li YP.,
R.	Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A A	Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pai G., Peterson J., Pham P.K., Rizzo M., Roonev T., Rowlev D.,
RA:	Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA E	Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Trtpochack T. Van Akon S. Vavchord M. Vycotekaja V.S. Walker M
<b>8</b> 8	Wu D., Yu G., Praser C.M., Venter J.C., Davis R.W.;
RT	"Sequence and analysis of chromosome 1 of the plant Arabidopsis
RI.	thaliana."; Nature 408:816-820(2000).
N.	
ማ ማ ር	SEQUENCE OF 3533-3681 FROM N.A.
Z X	PubMed=11910074; DOI=10.1126/science.1071006;
<b>8</b> 8	Seki M., Narusaka M., Kamiya A., Ishida J., Satou M., Sakurai T., Nakajima M., Bnju A., Akiyama K., Oono Y., Muramatsu M.,
RA.	Hayashizaki Y., Kawai J., Carninci P., Itoh M., Ishii Y., Arakawa T.,

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3647 TCFNQLDLPEYQSKEQLQERLLLAIHEASEGF 3678
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                                                                     Q6K3Y7
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                                             RESULT 2
Q6K3Y7
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                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 WFWXIXXXXXXXXXXXXXXXX PXYGFXYLXXXXXXXXXXXXXXXXXXXXXXXX 76
SIMILARITY: Contains 1 UBA domain.
SIMILARITY: Contains 1 ubiquitin-interacting motif (UIM) repeat.
CAUTION: Ref.2 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Ubiquitin (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> S (in Ref. 1).
A -> T (in Ref. 1).
N -> K (in Ref. 1).
L -> S (in Ref. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 135; DB 1;
Pred. No. 4.1e-16;
3; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ubiquitin in vitro
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EMBL; AC0023304; AAF79338.1; ALT SEQ.
EMBL; AK117912; BAC42550.1; ALT_INIT.
PIR; H96599; H96599.
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008938; ARM.
InterPro; IPR010309; DUF908.
InterPro; IPR010314; DUF913.
InterPro; IPR000569; HECT domain.
InterPro; IPR000499; UBA_domain.
InterPro; IPR003903; UIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conjugation pathway.
1269 1310 UBA.
1316 1335 UIM.
3340 3681 HECT
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Best Local Similarity 32.6%;
Matches 30; Conservative
                                                                                                                                                                                                                                 gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF06012; DUF908; 1.
Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF02809; UIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50237; HECT; 1.
PROSITE; PS50030; UBA; 1.
PROSITE; PS50330; UIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00119; HECTC; 1.
SMART; SM00165; UBA; 1.
SMART; SM00726; UIM; 1.
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1186
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3027
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3622 WFWEVVNGFSKEDMARFLQFVTGTSKVPLEGFKALQGISGPQRFQIHKAYGAPERLPSAH 3681
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Name-UPL2; OrderedLocusNames=At1g70320; ORFNames=F1707.14, F1707.15;
Arabidopsis thaliana (Mouse-ear cress).
Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                            Putative ubiquitin-protein ligase 1.

Name=P0574F11.30;
Oryza sativa (japonica cultivar-group).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UPL2 ARATH STANDARD; PRT; 3658 AA.

QBH0T4; O64604; O64605; Q9M7K6;

QBH0T4; O64604; Created)
25-OCT-2004 (Rel. 45, Last aquence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP005590; BAD22340.1; -... GO; GO:0005622; C:intracellular; IEA. GO; GO:0016874; F:ligase activity; IEA. GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA. GO; GO:0006512; P:ubiquitin cycle; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3716 AA; 408312 MW; 65C83DB881673FD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0574F11.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases
                                                                       Last sequence update)
Last annotation update)
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Pred. No. 4.2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCFNQLDLPEYSSKEQLEERLLLAIHEASEGF 3713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 TCFNXLDLPXYXSXXXXXXXXXXXXXXXXX 108
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                                                  Created)
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InterPro; IPR000569; HECT.
                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008938; ARM.
InterPro; IPR010309; DUF908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00632; HECT; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF02809; UIM; 1.
SMART; SM00119; HECTc; 1.
SMART; SM00165; UBA; 1.
PROSITE; PS50237; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF06012; DUF908; 1.
Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
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nes 30; Conservative
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InterPro; IPR003903; UIM.
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PS50330; UIM; 1
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=39947;
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ID UPL2_AR
AC 08H074.DT 25-0CT-1
DT 25-0CT-1
DT 25-0CT-1
DE 11gase
GN Name-Uf
CO Name-Uf
CO Spermat
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Matches 30; Conservative
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InterPro; IPR008938; ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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263
1759
1771
3298
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                                                                                                                                                                                                                    InterPro;
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MEDLINE=22954580; PubMed=14593172; DOI=10.1126/science.1088305;

A MEDLINE=22954580; PubMed=14593172; DOI=10.1126/science.1088305;

Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Miranda M., Quach H.L., Tripp M., Chan M.T., Yu G.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Chao Q., Choy M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Chao Q., Choy M., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Xamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 ubiquitin-interacting motif (UIM) repeat. CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
                                                                                                         Bates P.W., Vierstra R.D.;
PUD1 and 2, two 405 kDa ubiquitin-protein ligases from Arabidopsis
"Haliana related to the HECT-domain protein family.";
Plant J. 20:183-195(1999).
                                                             SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
STRAIN=cv. Columbia;
MEDLINE=20040063; PubMed=10571878;
SIMILARITY: Contains 1 UBA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 3298-3658 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:816-820(2000).
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                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
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3564 WFWEVVKAFSKEDMARFLÖFVTGTSKVPLEGFKALOGISGPORLOIHKAYGSPERLPSAH 3623
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Debaryomyces.
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Asp-rich.
Ublquitin (By similarity).
NL -> ES (in Ref. 1).
Q -> R (in Ref. 1).
Q -> R (in Ref. 1).
D -> N (in Ref. 1).
I -> F (in Ref. 3; AAN72076).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; 56A08EEFE02DA66D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similar to tr|Q03280 Saccharomyces cerevisiae D8035.1P.
ORFNames=DEHA0G06182g;
Debaryomyces hansenii CBS767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                   InterPro; IPR000569; HECT domain.
InterPro; IPR000449; UBA domain.
InterPro; IPR003903; UIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l conjugation pathway.
1271 1312 UBA.
1318 1337 UIM
1318 1358 HECT
2116 2210 Asp.
3625 3625 Ubic
                                                                          EMBL; AC003671; AAC18812.1; AL EMBL; AC003671; AAC18813.1; AL EMBL; BT002065; AAN72076.1; AL EMBL; BT008830; AAP68269.1; -- PIR; T01490; T01491.
                                                                                                                                                                                                                                                                                                                          Pfam; PF06612; DUF913; 1.
Pfam; PF06625; DUF913; 1.
Pfam; PF00627; UBA; 1.
Pfam; PF00809; UIM; 1.
SMART; SM00119; HECT; 1.
SMART; SM00156; UBA; 1.
PR0STIE; PS50237; HECT; 1.
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                                                        EMBL; AF127565; AAF36455.1;
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17 WFWXIXXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXXX78 76
      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE, PS50237; HECT; 1
PROSITE; PS50030; UBA; 1.
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Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
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SEQUENCE 4177 AA;
                                                                                                                                                                                                                                                                                                                         Submitted (JUN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                               Waterston R.;
Submitted (NOV-2001)
                                                                                                                                                                                                                     Submitted (OCT-2000)
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                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                          Waterston R.H.;
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Matches
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Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicolski M., Oztaer S., Ozier Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wichen P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
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STRAIN=Bristol N2;
Edwards J., Du H., Lamar B., Kemp K., Wohldmann P., Walker C.;
"The sequence of C. elegans cosmid Y67D8C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 132; DB 2; Length 3349;
Pred. No. 1.4e-15;
4; Mismatches 60; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005622; C:intraceliular; IEA.
GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO:0006512; P:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383078 MW; A42D8924F2637D78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y6708C.5.
Name=Y6708C.5; ORFNames=Y6708C.5;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3315 TCFNQIDLPAYESYETLRGSVLLAITEGHEGF 3346
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008938; ARM.
InterPro; IPR010309; DUF908.
InterPro; IPR010314; DUF913.
InterPro; IPR000569; HECT.
Pfam; PF06612; DUF908; 1.
Pfam; PF06625; DUF913; 1.
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Best Local Similarity 30.4%;
Matches 28; Conservative
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PROSITE; PS50237; HECT; 1
SEQUENCE 3349 AA; 3830'
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                                                                                                                                                                                                                                                                                   Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                     STRAIN=CBS767;
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WormPase; Y67DBC.5; CE31665.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006612; P:ubiquitin cycle; IEA.
InterPro; IPR008938; ARM.
InterPro; IPR010309; DUF908.
InterPro; IPR010309; DUF913.
InterPro; IPR000669; HECT.
InterPro; IPR000449; UBA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                        to the EMBL/GenBank/DDBJ databases
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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HSSP; Q9HOMO; 1ND7.
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Pubmed=12712197; DOI=10.1038/nature01554;

Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Wang S., Nairnov S., Purcell S., Rehman B.,
Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
A Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
Astange-Thomann M., Barrett R., Gherre S., Kamal M., Kamysselis M.,
Mauceli E., Bielke C., Rudd S., Frishman D., Kroken S., Cogoni C.,
A Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
A Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
A Rasmussen C., Jorbach M.J., Berglund J.A., Voelker R.,
DeSouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
Araden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
Nature 422:859-868(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Probable ubiquitin ligase protein, which may be involved in mRNA export. B3 ubiquitin ligase protein mediate ubiquitination and subsequent proteasomal degradation of target proteins. Participates in mRNA export from the nucleus by regulating the transport of hnRNP proteins (By similarity).

PATHWAY: Ubiquitin conjugation; third step.
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: Belongs to the TOMI/PTR1 family.
SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.";
Nucleic Acids Res. 31:1944-1954(2003).
                                                                                                                                                                                                                                                                                                                          Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                    25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin protein ligase TOMI-like protein (EC 6.3.2.-)
ORFNames=B11B22.010, NCU08501.1;
                                                           TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                4143 TCFNQLDLPQYESYEKLRQSLLLAI
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EMBL; AABX01000134; EAA34194.1; -.
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STRAIN=74-OR23-1A / FGSC 987;
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Wood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A James K., Jones L., Jones M., Lacther S., McDonald S., McLean J., James K., Jones L., Jones M., Lacther S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Olver K., O'Nell S., Parason D., Quall M.A., Rabbinowitsch E., Skelton J., Simmonds M., Squares R., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Taylor K., Taylor K., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aer R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aer R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Ber P., Zimmermann W., Wedler H., Wambut R., Purnelle B., Galfer R., Purnelle B., Galfer R., Rocke M., Rocket M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Jucas M., Rocket M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
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25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin protein ligase ptrl (EC 6.3.2.-) (Poly(A)+ RNA transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXX
                                                                                                                                                                                                              Coiled coil; Ligase; mRNA transport; Nuclear protein; Transport; Ubl conjugation pathway.

HECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 130; DB 1; Length 4065; Pred. No. 4.1e-15; 3; Mismatches 60; Indels (
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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
                                                                                                                                                                                                                                                                                                                                                                Ubiquitin (By similarity).
MW; F74683CEC36F9350 CRC64;
                                                                                                                                                                                                                                                                                 Coiled coil (Potential)
Coiled coil (Potential)
Coiled coil (Potential)
Coiled coil (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4031 TCFNQLDLPEYENYETLRSQLLKAITAGSDYF 4062
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                                                                                   IPR000569; HECT_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1).
Name=ptr1; ORFNames=SPAC19D5.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                   48.0%;
PIR; T49799; T49799.
HSSP; Q05086; 1C4Z.
InterPro; IPR010309; DUF908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 31.5%;
Conservative
                                                                   InterPro; IPR010314; DUF913
                                                                                                                                                                                                                                                                                                                                                                                           452568
                                                                                                         Pfam; PF06012; DUF908; 1.
Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
SMART; SM00119; HECTC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                        SMART; SM00119; HECTC; 1
PROSITE; PS50237; HECT;
                                                                                                                                                                                                                                                                                                      2568
2924
3369
4032
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2491 256
2839 292
3320 336
4032 403
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ses 29; Conserv
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ubiqitin ligase (Fragment).
ORFNames=YALI0B05940g;
                                                                                                                             Genolevures;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
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                                                                            PUNCTION, AND MUTANT PTR1-1.

PubMed=15094387; DOI=10.1016/j.bbrc.2004.03.171;

PubMed=15094387; DOI=10.1016/j.bbrc.2004.03.171;

PubMed=15094387; DOI=10.1016/j.bbrc.2004.03.171;

Andoh T., Azad A.K., Shigemateu A., Ohshima Y., Tani T.;

The fission yeast ptr1+ gene involved in nuclear mRNA export encodes a putative ubiquitin ligase.";

Biochem. Biophys. Res. Commun. 317:1138-1143(2004).

-I-FUNCTION: Probable ubiquitin ligase protein involved in mRNA export. B3 ubiquitin ligase protein mediate ubiquitination and subsequent proteasomal degradation of target proteins. Probably participates in mRNA export from the nucleus by regulating the transport of hnRNP proteins such as rael.

-I-SUBCELLUMAR LOCATION: Nuclear.

-I-SUBCELLUMAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asp-rich.
Ubiquitin (By similarity).
L->Q: In ptr1-1; induces defects in mRNA
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Last sequence update)
Last annotation update)
Saccharomyces cerevisiae YDR457w TOM1 E3
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                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the TOMI/PTR1 family. SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
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Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsbury Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakvoski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3227 AA; 365028 MW; 07FC47AB79124575 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF06612; DUF908; 1. Pfam; PF06025; DUF913; 1. Pfam; PF06025; DUF913; 1. SmART; SM00119; HECT; 1. PR0STTE, PS50237; HECT; 1. Ligase; mRNA transport; Nuclear protein; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.6%; Score 129; DB 1; 31.5%; Pred. No. 5.1e-15;
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GeneDB SPombe, SPAC19D5.04; -.
InterPro, IPR010309; DUF908.
InterPro, IPR010314; DUF913.
InterPro, IPR000569; HECT_domain.
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Q6CFL1;
25-OCT-2004 (TrEMBLrel. 28, C1
25-OCT-2004 (TrEMBLrel. 28, L6
25-OCT-2004 (TrEMBLrel. 28, L6
25-OCT-2004 (TrEMBLrel. 28, L6
Similarities with tr|Q03280 S6
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99531; CAB16714.1; -. PIR; T37964; T37964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugation pathway.
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1854
3194
                                                                                                                                                                                                                                                                                           domain.
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Q6CFL1
ID Q6CF
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3226 WFWRSIRSFDDÉERAKLLÓFVTGTSKVPLDGFKELEGMNGPTKFNÍHRAYGNNERLPSSH 3285
                                                                                                                                                                                                                                                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Lafontaine I. de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Agile M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Rabre E., Falrhead C., Ferry Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolaki M., Oztas S., Oztaer-Kalogeropoulos O.,
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A Caniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Buuchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
T., "Genome evolution in yeasts.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; CR382128; CAG82782.1; -...
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR08938; ARM.
InterPro; IPR010305; Armadillo.
InterPro; IPR010314; DUF913.
InterPro; IPR010314; DUF913.
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3320 AA; 369711 MW; CFC8C54DFA8C8C20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp564H223 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3286 TCFNQLDLPEYDSYETLRGSLLLAITEGREGF 3317
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                                                                      Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SMOOII; HECTE: 1.
PROSITE; PS50176; ARM REPEAT; 1.
PROSITE; PS50237: HPCT.
farrowia lipolytica CLIB99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF06012; DUF908; 1.
Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44(2004)
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les 30; Conserv
                                                                                                     NCBI_TaxID=284591;
                                                                                                                                                                        N.A.
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SEQUENCE FROM N.A.
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Query Match
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okazaki Y., Furuno M., Kasukawa T., Janana J., Bono H., Kondo S., A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa T., Nogami A., Schonbach C., Gojobori T., Balacelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Carinal L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brade D.A., Chothai L.E., Cousins S., Dalla E., Dragani T.A., Flercher C.F., Forrest A., Frazer K.S., Andrews J., Cariboldi M., Gissi C., Godzik A., Gough J., Annagia A., Karochkin I.V., Lee Y., Lenhard B., Lyons P.A., Magashima T., Numatas L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numatas K., Okido T., Pavan W.J., Pertea G., Peeole G., Petrovsky N., Pillai R., Ponttius J.U., Qi D., Ramachandran S., Andreide C., Seguple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Seguple C.A., Setou M., Shimada M., Sandelin A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
                                                                                                                                                                                                                                                                                                                                                                                                                     17 WFWXIXXXXXXXXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXLPXXH
                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 WFWQAVETFDEERRARLLQFVTGSTRVPLQGFKALQGAAGPRLFTIHLIDANTDNLPXAH
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-SOCT-2004 (Rel. 45, Last annotation update)
Smad ubiquitination regulatory factor 1 (BC 6.3.2.-) (Ubiquitin-protein ligase SMURF1) (Smad-specific E3 ubiquitin ligase 1)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  , Mewes H.W., Weil B., Amid C., Osanger A.,
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                                                                                                                                                                                                                                                                                                                                                             Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/63; TISSUE=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
                                                                                                                                                                                                                                                                                                                                                        47.2%; Score 128; DB 2; Length 29
31.8%; Pred. No. 7.5e-16;
ive 4; Mismatches 54; Indels
                                                                                                                                                                                          GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
                                                                                                                               Fobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ALB342-21; CAD38919.1; -.
HSSP; Q9HOMO; IND7.
                                                                                                                                                                                                                                                                                                                              295 AA; 34030 MW; 0507325127A943EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCFNXLDLPXYXSXXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The German cDNA Consortium;
                                                                                                                                                                                                                                                  Pfam, PF00632; HECT; 1.
SMART, SM00119; HECTC; 1.
PROSITE; PS50237; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 31.8
nes 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                 Wambutt R., Heubner D.
sapiens (Human).
                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                       SEQUENCE FROM N.A.
                                           NCBI_TaxID=9606;
                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
Name=Smurf1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
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Matches
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SUF1_MOUSE
ID GOUN'S
BDT 28-FE
DT 28-FE
DE Smad
OC Mamma
RA Dalla
RA Balda
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RA Kanai
RA RA Sanda
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Wilming L.G., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yung I., Zhu Y., Zin Y., Zinmer A., Carninci P., Hayatsu N., A Hrozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakzu N., Aniraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Ahraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Ashiraki T., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Asunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Analysis of the mouse transcriptome based on functional annotation of G. 770 full-length cDNAs.";

Nature 420:553-573 (2002).

C. - FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates.

C. Interacts with receptor-regulated SMADS specific for the BMP pathway, SMAD1 and SMADS, in order to trigger their ubiquitination and degradation and hence their inactivation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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MGD; MGI:1923038; Fubfiguitin-protein ligase activity; ISS.
GO; GO:0004842; Fubfiguitin-protein ligase activity; ISS.
GO; GO:0001984; P:cell differentiation; ISS.
GO; GO:0007398; P:cetoderm development; ISS.
GO; GO:0007398; P:protein development; ISS.
GO; GO:0042787; P:protein ubiquitination of BMP signaling pathway; ISS.
GO; GO:0006512; P:ubiquitin cycle; ISS.
InterPro; IPR000008; C2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Ubiquitin conjugation; third step.
-!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
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Pfam; PR001202; WW.Rsp5_WWP.
Pfam; PR001303; HECT.
IGRPAMS; TIGR01847; 1.
PR051TE; PS010499; C2_DOMAIN.1; PĀRTIAL.
PR051TE; PS501049; C2_DOMAIN.1; PĀRTIAL.
PR051TE; PS501159; WW DOMAIN.1; 1.
PR051TE; PS501159; WW DOMAIN.1; 1.
PR051TE; PS501159; WW DOMAIN.1; 1.
PR051TE; PS501019; WW DOMAIN.1; 1.
PR051TE; PS501019; WW DOMAIN.1; 1.
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WW 2.
HECT.
POly-Gly.
Ubiquitin (By similarity).
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4; Mismatches
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Les 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                               STRAIN-CZECH II; TISSUE=Manmary tumor;

STRAIN-CZECH II; TISSUE=Manmary tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Bwagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Tapletcon M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1923038; Smurfl.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:000612; P:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CZECH II, TISSUE=Mammary tumor;
Director MGC Project;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 C2 domain.
EMBL; BC029097; AAH29097.1; -.
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                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Smad ubiquitination regulatory factor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                  Created)
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000008; Č2.
InterPro; IPR008973; C2. CalB.
InterPro; IPR001505; WW.Rsp5_WWP.
Pfam; PP00168; C2; 1.
Pfam; PP00612; HECT; 1.
Pfam; PP006397; WW; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00499; C2 DOMAIN 1; 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50237; HEGT; 1.
PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 2.
SEQUENCE 728 AA; 83083 MW; C3:
                                                                                               01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00239; C2; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 2.
                                                 PRELIMINARY;
                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                  SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                 Q8K300
RESULT 11

084300

084300

DT 001-0C

DT 01-0C

DT 01-0C

DT 01-0C

DT 01-0C

DT 01-0C

DT 01-0C

DE Smach

RN Mus mm

CO Rukar

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OC Rukar

OC Rukar

OC Rukar

OC Rukar

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RN Klaus

RA Hoks

RA Hoks

RA Hoks

RA Hoks

RA Blake

RA Fahey

RA Raha

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RA Raha

RA Raha

RA Blake

RA Raha

RA Piche

RA Blake

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                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO51489; AAH51489.1; -.
HSSP; Q9H0M0; JND7.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; F:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 AA; 15188 MW; A45D5569533F7E09 CRC64;
                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to E3 ubiquitin ligase SMURF2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                     133 AA.
                                                                                  695 TCFNRIDIPPYESYEKLYEKLLTAV 719
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                                                   77 TCFNXLDLPXYXSXXXXXXXXXXX 101
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                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 32.5%,
Sest Local 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00632; HECT; 1.
PROSITE; PS50237; HECT; 1.
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                     RESULT 12
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Similarity 31.8 27; Conservative

Local

Matches

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Gaps

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TISSUE-Mammary gland;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METAGENER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Datchenco, L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

McKrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, BC065796, AAH65796.1; -
GO, GO:0005622; C:intracellular, IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
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                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A. 99:16899-16903(2002)
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32.9%; Pred. No. 7.6e-16;
iive 3; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000569; HECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse cDNA sequences.
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary gland;
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                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Q9CSE3
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OF THE STANDARD STANDARD SOLUTION OF THE STAND
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258 AA.

PRT;

PRELIMINARY;

Q9CSE3

Q9CSE3; 01-JUN-2001 (TrEMBLrel. 17, Created)

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GYRAIN-C57BL/6J; TISSUE-Whole body;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramock T., Hiraoka T., Hori F.,
Marayama T., Hori P., Tawa M., Kasukawa T., Kato H.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sasito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Bubmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BEBL; AKO1302; BAB28637.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ECSPEL(60; TISSUE-Whole body;
MEDLINE-20499374; PubMed-11042159;
MEDLINE-20499374; PubMed-11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Whole body; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hispahlazki Y.; Hispahlazki Y.; Hispahlazki Y.; Mispahlazki Y.; Mispahlazki Y.; Mispahlazki Y.; Mispahlazki Y.; Meth. Enzymol. 303:19-44(1999).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810411B22 product:similar to SIMILAR TO E3
UBIQUITIN LIGASE SMURF2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunin H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Macsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Isawa M., Ohara E., Watsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rikik ihregatated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM CONSORTIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1913563; Smurf2
                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q9H0M0; 1ND7.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                    Name=Smurf2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 WFWXIXXXXXXEXXXXXQFXTGXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXX 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 127; DB 2; Length 258; 32.9%; Pred. No. 1e-15; live 3; Mismatches 54; Indels
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPRO00569; HECT.
FRAMER; SM00119; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung;
Director MGC Project;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC009527; AAH09527.1; -.
HSSP; Q9H0M0; 1ND7;
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004621; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
                                                                                                                                                                                                                                                                                                                                                                                                  258 AA; 29670 MW; BOBE04BCE1FCBC98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 TCFNXLDLPXYXSXXXXXXXXXX 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                               PROSITE, PSS0237; HECT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 32.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                 TER
                                                                                                                                                                                                                                                                                                                                Ligase.
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195 WFWKAVEFFDEERRARLLQFVTGSSRVPLQGFKALQGAAGPRLFTIHQIDACTNNLPKAH 254
                                                                                                                17 WFWXIXXXXXXXXXXXXXXXXXXRLPXXGFXXLXXXXXXXXXXXXXXXXXXXXXX 76
                                                                                         Gaps
                                                                                         .;
0
                                                               Length 288;
                                                                                         Indels
                                      SEQUENCE 288 AA; 33255 MW; FE2B43E300E66537 CRC64;
                                                     46.9%; Score 127; DB 2; Le
32.9%; Pred. No. 1.1e-15;
                                                                                                                                                                    77 TCFNXLDLPXYXSXXXXXXXXXXX 101
                                                                                                                                                                                            255 TCFNRIDIPPYESYEKLYEKLLTAI 279
SMART; SM00119; HECTC; 1.
PROSITE; PS50237; HECT; 1.
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completed: October 13, 2005, 15:09:12 ne : 208.714 secs

Search co

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October 13, 2005, 14:01:04; Search time 74.3407 Seconds (without alignments) 171.684 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                        - protein search, using sw model
                       Copyright
                                                                                        OM protein
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Title: Perfect score:	US-09-385-918-2 129
Sequence:	1 GPLPXGWEXXXXXXXXXXXYYXXHNTXTTXWXXPX 33
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues
Total number of	Total number of hits satisfying chosen parameters: 2105692

cers: 2	
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chosen	0
Total number of hits satisfying chosen parameters:	Minimum DB seg length: 0 Maximum DB seg length: 200000000
hits	length:
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numbe	n DB
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Post-processing: Minimum Maximum Listing	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	A_Geneseq_16Dec04:* 1: geneseqp1990s:* 3: geneseqp2090s:* 4: geneseqp2000s:* 5: geneseqp2001s:* 6: geneseqp2001s:* 7: geneseqp2003bs:* 7: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Length DB ID De	.0 33 4 AAB83017 Aab83017 Human HEC	37	38 5 AAU87962 Aau87962	38 7 ADB49230 Adb49230	1082	33 2 AAW38107 Aaw38107	33 7 ADB49233	759 6	869 6 ABJ26104 Abj26104	38 2 AAR97685 Aar97685	38	38 4 AAB83024 Aab83024	38 5 AAU87968 Auman			766 2 AAW13385 Aaw13385	832 5 ABP73459 Abp73459 Candid	870 4 AAE05495	870	.3 870	.3 870 8 ABM81770 Abm81770	.3 906 2 AAW36795 Aaw36795	. 906 .	COURT CONTRACTOR CONTR
di	Query Match	76.	75.	75.	75.	73.6	72.	72.	72.	72.	71.	71.3	71.	71.3	71.3	71.3	71.3	71.3	71.	71.3	71.	71.	71.	71.	7
	Score	96	97	76	97	95	93	93	93	93	92	92	92	92	92	92	92	92	92	92	92	92	92	92	5
	Result No.		7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	•

Aab21979 RSPS/9C p	Aab83022 Yeast Rsp		Adb49232 Novel hum	Adb49213 Yeast WW	Aaw36796 Novel hum	Adb49244 Novel hum	Aar97679 Mouse Yes	Adb49210 Mouse WW	Adb49208 Chicken W	Novel	Novel	Aar97672 Mouse Yes	Aar97684 Yeast Rsp	Aab83023 Yeast Rsp	Adb49216 Yeast WW	Aay10943 Amino aci	Adb47966 Novel hum	Adj55521 Novel hum	Novel
AAB21979	AAB83022	AAU87971	ADB49232	ADB49213	AAW36796	ADB49244	AAR97679	ADB49210	ADB49208	ABG06171	ABG14510	AAR97672	AAR97684	AAB83023	ADB49216	AAY10943	ADB47966	ADJ55521	ABG16477
38 3	38 4	38 5	38 7	38 7		. 42	38 2	38 7	38 7	132 4	192 4	470 2		38 4	38 7		-	474 8	739 4
70.5	70.5	70.5	70.5	70.5	70.5	70.5	69.8	69.8	8.69	69.8	69.8	69.8	0.69	69.0	69.0	0.69	0.69	0.69	0.69
91	91	91	91	91	91	91	6	06	6	8	90	06	83	83	89	89	89	83	89
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Misc-difference 12. .14
/label= Ser, His, Pro, Asp, Glu, Thr, Tyr
/note= "each residue is an independently selected polar
                                                                                                                                                                                                                                                                                                                  Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid"
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/note= "independently selected polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid"
                                                                                                                                                                                                                                                 Human HECT E3 ubiquitin ligase WW domain consensus sequence.
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/note= "independently selected polar amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ser, His, Pro, Asp, Glu, Thr, Tyr
/note= "independently selected polar amino
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/label= Ser, His, Pro, Asp, Glu, Thr, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9. .11
/note= "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note⇒ "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Xaa = any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Xaa = any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Ile, Val, Leu, Met/note= "hydrophobic residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers Misc-difference 5
                              AAB83017 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid"
                                                                                                                                                              25-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                      AAB83017;
AAB83017
                                     THE STATE OF THE S
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Fowlkes DM;

Kay BK,

97WO-US005547.

96US-00630916.

CYTOGEN CORP. UNIV NORTH CAROLINA.

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Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful
                                                                                                                                                                                                                                                                               in targetted drug selection.
                                                                                                                                                                                                   WPI; 1997-503234/46
                    3-APR-1997;
                                                            03-APR-1996;
                                                                                                                                                             Pirozzi G,
                                                                                                   (CYTO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase WW domain. The WW domain binds to the Smad PY motif, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating choren bones, osteoporosis, and acute or chronic renal failure. Agents that that inhibit TGF-mediated signalling are useful for treating cancer, that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; WWP4.
                                                                                                                                                                                                                                                                                                                                                                             Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                       /label= Ser, His, Pro, Asp, Glu, Thr, Tyr
/note= "independently selected polar amino acid"
/note= "independently selected polar amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 98; DB 4; L Pred. No. 5.3e-10;
                                                                                                                                                                                                                                                                                                  Mercurio FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                  Murray BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 34; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide containing a WW domain.
                                                                                                                                                                              29-AUG-2000; 2000WO-US023729.
                                                                                                                                                                                                                     99US-00385918.
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                                                                                                                                                                                                                                                             (SIGN-) SIGNAL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                  Hoekstra MF, Xie W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conserva
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-327913/34.
                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 AA;
                                                                                                   WO200116604-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-1998
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comples AAW36799-801 and AAW37636-40 are peptides that contain WW domains. The WW domain is a small functional domain found in a large number of proteins from a variety of species including humans, nematodes and yeast. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW commain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug interactions. The valency of the recognition unit is important in determining specificity of interaction with WW domains. In multivalent form specificity is relaxed, but not lost, so proteins containing WW domains similar, but not identical, to the sequence of the peptides' target WW can be detected, including new polypeptides
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Claim 49; Page 104; 220pp; English.
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28-NOV-2000; 2000US-00723810.
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nes 17; Conserv
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ABB63355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the
                                                                                                                         The invention relates to methods for identifying polypeptides comprising PDZ domains, and their encoding nucleic acids. The sequences are used to identify modulators of their expression, function and activity, for use in the diagnosis and treatment of PDZ related disorders. Antibodies against the proteins and cells that produce them may be used for the treatment of PDZ-mediated disease states. Sequences AAU87843-AAU87974 represent proteins containing PDZ domains, fragments of these proteins and other related peptides used in the methods of the invention
                                                            Methods for identifying polypeptides comprising PDZ domains, the polypeptides and their encoding nucleic acids, useful for the diagnosis and treatment of PDZ related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein 2; WWP2; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
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                                                                                                                                                                                                                                             75.2%; Score 97; DB 5; Length 38; 53.1%; Pred. No. 9.3e-10;
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0; Mismatches 15
                                                                                                                                                                                                                                                                                                           1 GPLPPGWEKRYDPNGRVYYVDHNTRTTWEDP 32
                                                                                                                                                                                                                                                                                        Novel human WWP2-3 protein WW domain.
                                                                                                       Disclosure; Fig 20; 225pp; English.
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(AXCE-) AXCELL BIOSCIENCES CORP.
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                                                                                                                                                                                                                                                                                                                                                                 ADB49230 standard; peptide; 38
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97US-00826516.
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                  17; Conservative
                    J, Pirozzi G,
                                                                                                                                                                                                                                                         Best Local Similarity
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(FOWL/) FOWLKES D M.
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                                        WPI; 2002-195842/25
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(KAYB/) KAY B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003077577-A1.
                                                                                                                                                                                                                         Sequence 38 AA;
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specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activaties, or as an immunogen to generate antibodies. This is the amino acid sequence of novel human WW binding protein WWP2-3 WW domain.
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9.3e-10;
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Pred. No. 9.3e-
0; Mismatches
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53.1%;
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.1'
Matches 17; Conservative
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Pirozzi
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                                                                                                                                                                                        Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator;
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                                          Gaps
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                         Length 1082;
                                         15; Indels
                        DB 4; L
8.5e-08;
                                                                          GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDP 686
                                                        1; Mismatches
                         Score 95;
Pred. No. 8
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                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                     AAW38107 standard; peptide; 33
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                       73.6%;
50.0%;
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                                                                                                                                                                        domain consensus sequence
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UNIV NORTH CAROLINA.
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                                          Conservative
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                        Query Match
Best Local Similarity
Matches 16; Conserv
         Sequence 1082 AA;
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Homo sapiens
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The present sequence is a consensus WW domain sequence. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan residues, one in the aminor terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most

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proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton.

Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW domain; drug candidate screening; drug discovery; drug drug refinement; immunogen; WW binding protein; WW domain.
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                                                                                                                                                                                                                                                          Pred. No. 4.1e-09;
                                                                                                                                                                                                                                      72.1%; Score 93; DB 2; 70.0%; Pred. No. 4.1e-09
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                       3 LPXGWEXXXXXXXXXXXXXXXXXXX 32
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97US-00826516.
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                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PIRO/) PIROZZI G.
(KAYB/) KAY B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOWLKES
                                                                                                                                                                                             Sequence 33 AA;
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03-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or inhibit formation on a surface of a by A. fumigatus, or to prevent or inhibit formation on a surface of a by A. fumigatus, or to prevent or inhibit formation on a surface of a capressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic transmisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or parabogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination
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activities, or as an immunogen to generate antibodies. This is the amino acid sequence of a WW domain binding protein associated protein. Note: This sequence appears in the sequence listing but is not further described in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
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                                                                                                                               Length 33;
                                                                                                                                                                   9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Aspergillus fumigatus essential gene protein #162.
                                                                                                                           Score 93; DB 7; 1
Pred. No. 4.1e-09;
0; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                    ABJ25504 standard; protein; 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-029590P.
09-JUL-2001; 2001US-0316399P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                               72.1%;
70.0%;
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                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fungicide; cytostatic;
cancer; contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-093124/08
                                                                                                                                                Similarity
                                                                                          Sequence 33 AA;
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                                                                                                                       Query Match
Best Local Simi:
Matches 21;
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The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergilus funigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. funigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. funigatus. The polynucleotides are useful for expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA similar biochemical activity and/or function, for comparing with DNA similar biochemical activity and/or function, for comparing with DNA similar brothemical activity and/or function; for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and
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with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
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                                                                                                                                                                                                                      Length 759
                                                                                                                                                                                                                                                            16; Indels
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                                                                                                                                                                                                                                                                                                                         32
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                                                                                                                                                                                                                                                                                                 GPLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP
                                                                                                                                                                                                                      Score 93;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ26104 standard; protein; 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                      72.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic;
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                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-093124/08.
                                                                                                                                                                               Sequence 759 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fungicide;
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Length 38;

Query Match

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                                              response, and for identifying polymucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypepides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes
 for examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Yes proto-oncogene associated protein - used to modulate intracellular signal transduction e.g. for treatment of muscular
                                                                                                                                                                                                                                                                                                          Gaps
making oligomers for attachment to a nucleic acid array for examina of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune
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Pred. No. 1.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW domain; signal transduction; diagnosis; gene therapy;
Yes proto-oncogene associated protein; YAP; Rsp5.
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(DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.
                                                                                                                                                                                                                                                                                                                                                                             GRLPAGWERREDNLGRTYYVDHNTRTTTWTRP 314
                                                                                                                                                                                                                                                                                                                                             1 GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                 Aspergillus fumigatus of the invention
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                                                                                                                                                                                                                                                                  72.1%;
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95US-00476509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                          16; Conservative
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                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                      Sequence 869 AA;
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07-JUN-1995;
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Sequence 38 AA,

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comples AAW36798-801 and AAW37636-40 are peptides that contain WW domains. The WW domain is a small functional domain found in a large number of proteins from a variety of species including humans, nematodes and yeast. Its name is derived from the observation that two tryptophan residues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth requiation or the organisation of the cytoskeleton. Polypeptides containing a WW commain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domains are used for targeted drug screening, i.e. to identify who domains are used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions. The valency of the recognition unit is important in determining specificity of interaction with WW domains. In multivalent commains similar, but not identical, to the sequence of the peptides' target WW can be detected, including new polypeptides
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                                                                                                                                                                                                                                                                                                                                             WW domain; cell signalling; growth regulation; cytoskeleton organisation;
targeted drug screening; modulator; WW domain interaction; WWP4.
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                                     Indels
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   DB 2; L
7.2e-09;
                                                                          1 GPLPXGWEXXXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                        GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 32
Score 92; DB 2; Pred. No. 7.2e-1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fowlkes DM;
                                                                                                                                                                                                   AAW37637 standard; peptide; 38
                                                                                                                                                                                                                                                                                                          Peptide containing a WW domain.
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   71.3%;
46.9%;
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                    Best Local Similarity 46.99
Matches 15; Conservative
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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PLPPGWEKRTDPRGRFYYVDHNTRTTTWQRP 32

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Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                        Yeast, HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Rsp5.
                                                                   Yeast Rsp5 HECT E3 ubiquitin ligase WW domain #3
                                                                                                                                                                                                                                                                                                                 Mercurio FM;
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 14; 75pp, English.
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                                                                                                                                                                                                                                                                                                                Murray BW,
AAB83024 standard; peptide; 38
                                                                                                                                                                                                                                            29-AUG-2000; 2000WO-US023729.
                                            (first entry)
                                                                                                                                                                                                                                                                                          (SIGN-) SIGNAL PHARM INC.
                                                                                                                                                                         Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                Hoekstra MF, Xie W,
                                                                                                                                                                                                                                                                                                                                       WPI; 2001-327913/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38 AA;
                                                                                                                                                                                               WO200116604-A1
                                                                                                                                                                                                                                                                   30-AUG-1999;
                                             25-JUN-2001
                                                                                                                                                                                                                     08-MAR-2001
                        AAB83024;
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The present sequence is the WW domain of a HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase. The WW domain binds to the Smad PY motif, resulting in ubiquitination of Smad by the E3 ubiquitin ligase.

The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for treating concer, signalling are useful for treating cancer, that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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Gaps
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  Length 38;
                        Indels
71.3%; Score 92; DB 4;
46.9%; Pred. No. 7.2e-09;
ive 1; Mismatches 16
                          Conservative
            Similarity
15; Conserv
 Query Match
              Best Local
                        Matches
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1 GPLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32

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GPLPSGWEMRLINTARVYFVDHNTKTTTWDDP 32
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Human, PDZ domain, WW domain, rat, cow, mouse, fruitfly, protein therapy, gene therapy, PDZ-mediated disease, inward potassium channel, WBP, dimer inhibitor peptide, carboxylate binding loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to methods for identifying polypeptides comprising PDZ domains, and their encoding nucleic acids. The sequences are used to identify modulators of their expression, function and activity, for use in the diagnosis and treatment of PDZ related disorders. Antibodies against the proteins and cells that produce them may be used for the treatment of PDZ-mediated disease states. Sequences ANUR97843-AANUR9794 represent proteins containing PDZ domains, fragments of these proteins and other related peptides used in the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods for identifying polypeptides comprising PDZ domains, the polypeptides and their encoding nucleic acids, useful for the diagnosis and treatment of PDZ related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein 2; WWP2; human.
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ches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.3%; Score 92; DB 5;
51.6%; Pred. No. 7.2e-09
cive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLPPGWEKRTDPRGRFYYVDHNTRTTTWQRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human WWP2-2 protein WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 20; 225pp; English
                 standard; peptide; 38 AA
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                                                                                                                                                                                                                                                                                                                                                                                          Uveges A;
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                                                                                                                                                                                                                                                                                                               25-JUL-2000; 2000US-0221215P. 28-NOV-2000; 2000US-00723810.
                                                                                                                                                                                                                                                                                   24-JUL-2001; 2001WO-US023269
                                                                        05-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-195842/25
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Best Local Similarity
Matches 16; Conserv
                                                                                                       Human WW domain #6.
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                                                                                                                                                                                                                        WO200207751-A1.
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                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                       31-JAN-2002.
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                                            AAU87968;
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               AAU87968
RESULT 14
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ID ADB4
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completed: October 13, 2005, 15:00:30 ne : 75.3407 secs
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                                                                                                                                                                                                                                                                                       The invention describes a purified polypeptide (I) comprising a Ww domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the Ww domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and activaties, or as an immunogen to generate antibodies. This is the amino acityties, or as an immunogen to generate antibodies. This is the amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein; yeast; Rsp5; WW domain.
                                                                                                                                                                                               Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
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Best Local Similarity 51.6%; Pred. No. 7.2e-09;
Matches 16; Conservative 0; Mismatches 15,
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                                                                                                                                              Fowlkes DM
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97US-00826516.
                        28-JUN-2002; 2002US-00185050.
                                                   96US-00630916.
97US-00826516.
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                                                                                                                   (FOWL/) FOWLKES D M.
                                                                                                                                              Pirozzi G, Kay BK,
                                                                                                                                                                        WPI; 2003-635075/60.
                                                                                        (PIRO/) PIROZZI G.
(KAYB/) KAY B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003077577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38 AA;
                                                   03-APR-1996;
03-APR-1997;
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03-APR-1997;
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                                                                                                                                                                                                                                         antibodies.
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The invention describes a purified polypeptide (1) comprising a Ww domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (1) is useful for screening a potential drug candidate, by allowing (1) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (1), in the presence of an amount of a potential charge candidate, such that (1) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the amount of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (1) with the recognition unit. (1) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogent to generate antibodies. This is the amino
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Matches 15; Conservative
                                       KAY B K.
FOWLKES D M.
                                                                                                                                                                                                         WPI; 2003-635075/60
                                                                                                                                        Kay BK,
PIROZZI G.
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   (PIRO/)
(KAYB/)
                                                                                                                                            Pirozzi
                                                                        (FOWL/)
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October 13, 2005, 13:59:34; Search time 70.3516 Seconds (without alignments) 195.471 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUDLISHER APPLICATIONS AND TO THE COME. DEPT. 1. (1902 6/ptodata1/pubpaa/USO7_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO6_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO6_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO6_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO7_NEW_PUB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO8_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO8_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO8_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO8_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO9_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO0_PUBCOMB. DEPT. 1. (1902 6/ptodata1/pubpaa/USO0_NEW_PUB. DEPT. 1. (1902 6/ptodata1/pubpaa
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1859788 seqs, 416717961 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                    OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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	מסייייים מיייים		Sequence 2, Appli	Seguence 36, Appl	Seguence 158, App	Sequence 16857, A	Sequence 39, Appl	Sequence 3162, Ap	Sequence 8162, Ap	Sequence 26, Appl	Sequence 35, Appl	Sequence 9, Appli	Sequence 164, App
	C		US-10-307-956-2	US-10-185-050-36		US-11-097-143-16857	US-10-185-050-39	US-10-128-714-3162	US-10-128-714-8162	US-10-185-050-26	US-10-185-050-35	US-10-307-956-9	US-10-785-819-164
	9	:	14	14		20	14	14	14	14	14	14	17
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### ALIGNMENTS

RESULT 1

US-10-307-956-2

US-10-307-956-2

1 US-10-307-956-2

Sequence 2, Application US/10307956

Publication No. US20030119072A1

Sequence 2, Application US/20030119072A1

Sequence 2, Application No. US20030119072A1

GENERAL INFORMATION:

APPLICANT: Xie, Wellin

APPLICANT: Mercurio, Frank

TITLE OF INVENTION: METHORY FOR MODULATING SIGNAL

TITLE OF INVENTION: METANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS

TITLE OF INVENTION: METANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS

TITLE OF INVENTION: METANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS

TITLE OF INVENTION: METANSCH WEST US/09/385,918

PRIOR FILING DATE: 1924-04\_30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 3

TYPE: PRT

NAME/KEY: VARIANT

LOCATION: (9)...(1)

OTHER INFORMATION: Xaa = any amino acid

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(14)

OTHER INFORMATION: Xaa = independently selected polar amino acid

FEATURE:

NAME/KEY: VARIANT

LOCATION: (12)...(14)

OTHER INFORMATION: Xaa = independently selected polar amino acid

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RESULT 3

US-10-785-819-158

Sequence 158, Application US/10785819

Publication No. US2005011252A1

GENERAL INFORMATION:

APPLICANT: Herrero.

APPLICANT: Pirzzi, G.

TITLE OF INVENTION: DENTIFICATION AND ISOLATION OF NOVEL

TITLE OF INVENTION: POLYPEPTIDES HAVING PDZ DOWAINS AND METHODS OF USING SAME

TITLE OF INVENTION: POLYPEPTIDES HAVING PDZ DOWAINS AND METHODS OF USING SAME

CURRENT PILICATION NUMBER: US/09/723,819

CURRENT FILING DATE: 2004-02-23

PRIOR APPLICATION NUMBER: US/09/723,810

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 170

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 158
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISRATON:
NAME: MISRATON NUMBER: 18 872
REFERENCY/DOCKET NUMBER: 1101-208-999
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (212) 790-9090
TELEFAX: (614) PENNIE
INFORMATION FOR SEQ 1D NO: 36:
SEQUENCE CHARACTER:STICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 38 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.1%
watches 17; Conservative
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CRGANISM: Homo Sapiens
US-10-785-819-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-097-143-16857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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              OTHER INFORMATION: Xaa = independently selected polar amino acid OTHER INFORMATION: (e.g., S,H,P,D,E,T or Y)
NAME/KEY: VARIANT
LOCATION: (**COMMANDER COMMAND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (31)...(31)
OTHER INFORMATION: Xaa = independently selected polar amino acid
OTHER INFORMATION: (e.g., S,H,P,D,E,T or Y)
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OTHER INFORMATION: Xaa = independently selected polar amino acid
OTHER INFORMATION: (e.g., S,H,P,D,E,T or Y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (25)...(25)
OTHER INFORMATION: Xaa = independently selected polar amino acid
OTHER INFORMATION: (e.g., S,H,P,D,E,T or Y)
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OTHER INFORMATION: Xaa = independently selected polar amino acid
OTHER INFORMATION: (e.g., S,H,P,D,E,T or Y)
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OTHER INFORMATION: Xaa = hydrophobic residue (e.g., I,V,L or M)
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ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPLPXGWEXXXXXXXXXXXXHNTXTTXWXXP 32
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OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                             ION: (17)...(17)
INFORMATION: Xaa = any amino acid
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OTHER INFORMATION: Xaa = any amino acid
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Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
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NAME/KEY: VARIANT
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NAME/KEY: VARIANT
LOCATION: (33)...
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid."
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid."
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid."
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid.
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OTHER INFORMATION: /note= "A Hydrophobic Amino Acid.
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OTHER INFORMATION: /note= "A Hydrophobic Amino
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Pred. No. 2.8e-08;
O; Mismatches 9;
                  REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
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                                                                                     TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note=
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OTHER INFORMATION: /note=
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Publication No. US20030119013A1
GENERAL INFORMATION:
APPLICANT: Uiang, Bo
APPLICANT: Hu, Wenqi
                                                                                                INFORMATION FOR SEQ 1D NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acide TYRE: amino acide STRANDEDNESS: «Unknown MOLECULE TYPE: peptide FEATURE:
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NAME: MISROCK, S. LESLIE
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70.0%;
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OTHER INFORMATION:
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Best Local Similarity
Matches 21; Conserv
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S-20-10-39
Sequence 39, Application US/10185050
Sublication No. US20030077577A1
GENERAL INFORMATION:
Kay, Brian K.
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                 APPLICANIT: PURENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 00/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SCOTT NA 16-67
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ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/185,050

FILING DATE: 28-Jun-2002

CLASSIFTANTION: CURKNOWN>
PRIOR APPLICATION NUMBER: US/08/826,516

FILING DATE: 03-APP-1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 GPLPEGWEERVHTDGRVFYIDHNTRTTOWEDP 686
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ADDRESSE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
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                       Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-097-143-16857
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us-09-385-918-2.rapb

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Sequence 35, Application US/10185050
Sequence 35, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDBNTIFICATION AND ISOLATION OF NOVEL
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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46.9%; Pred. No. 4.7e-08;
ive 1; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
                                                                        283 GRLPAGWERREDNLGRTYYVDHNTRTTTWTRP 314
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTATION OF A TOTAL COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-UMN-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                         1 GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown)

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-185-050-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                       US-10-185-050-26; Sequence 26, Application US/10185050; Publication No. US20030077577A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 46.9°
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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            APPLICANT: Zamudio, Carlos
APPLICANT: Erashkin, Alaxey M
APPLICANT: Lemieux, Sebaction of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REPERBRUE: 1018-299
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
FRIOR APPLICATION NUMBER: US 60/285,697
FRIOR APPLICATION NUMBER: US 60/285,890
FRIOR APPLICATION NUMBER: US 60/295,890
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-06-05
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTYON: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTYON: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR PLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
NUMBER OF SEQ ID NOS: 8603
NUMBER PACHALLATION NUMBER: US 60/316,362
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Pred. No. 6.2e-07;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93; DB 14; Length 75
Pred. No. 5.4e-07;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GRLPAGWERREDNLGRTYYVDHNTRTTTWTRP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8162, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION: APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Aspergillus fumigatus US-10-128-714-3162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Aspergillus fumigatus
US-10-128-714-8162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%;
Matches 16; Conservative
Tishkoff, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM:
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Best Local
APPLICANT
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Matches
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16; Conservative

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1; Mismatches
       Conservative
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ORGANISM: Homo Sapiens
US-10-785-819-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                   RESULT 11 US-10-785-819-164
       15;
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     Matches
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APPLICANT: Xie, Weilin
APPLICANT: Xie, Weilin
APPLICANT: Murray, Brion
APPLICANT: Murray, Brion
APPLICANT: Mercurio, Frank
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 860098 433
CURRENT APPLICATION NUMBER: US/10/307,956
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                       COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BEA FORM:

GOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,050

FLING DATE: 28-Jun-2002

CLASSIFCATION OBTA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/826,516

FILING DATE: 03-Apr-1997

ATTORNEY/AGENT INFORMATION:

NAME: MISROCK, S. LEGLIE

REFERRATION NUMBER: 1101-208-999

TELEFONDUMICATION INFORMATION:

SEQUENCE CHAIPENNIE

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 38;
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Pred. No. 4.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.3%; Score 92; DB 14;
51.6%; Pred. No. 4.7e-08;
tive 0; Mismatches 15
NUMBER OF SEQUENCES: 233
CORRESPONDENCE PUBDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PLPXGWEXXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PLPPGWEKRTDPRGRFYYVDHNTRTTTWQRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acide

TYPE: amino acide

STRANDEDNESS: «Unknown»

TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-185-050-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccharomyces cerevisiae US-10-307-956-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10307956 Publication No. US20030119072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.3%;
46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.6
Matches 16; Conservative
                                                                                               CITY: New York
STATE: New York
                                                                                                                                                  USA
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Best Local Similarity
                                                                                                                                                  COUNTRY:
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Sequence 164, Application US/10785819
Publication No. US20050112552A1
GENERAL INFORMATION:
APPLICANT: Herrero J
APPLICANT: Pirozzi, G.
APPLICANT: Uveges, A.
TITLE OF INVENTION: POLYPEPTIDES HAVING PDZ DOMAINS AND METHODS OF USING SAME;
FILE REPERENCE: 1101-211
CURRENT APPLICATION NUMBER: US/10/785,819
PRIOR PILING DATE: 2004-02-23
PRIOR PILING DATE: 2004-11-28
PRIOR PILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 170
SOFTWARE PASSED for Windows Version 4.0
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Gaps
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Publication No. US20030199036A1
GENERAL INFORMATION:
APPLICANT:
Beach, David H.
Caligiuri, Maureen
Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: One Post Office Square
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COUNTY: USA
COMPUTER READABLE FOORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 05-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 08/539,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 38;
  Indels
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  16;
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Best Local Similarity 51.6%; Pred. No. 4.7e-08;
Matches 16; Conservative 0; Mismatches 15;
                                            ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matchew P.
REGISTRATION UNMBER: 36, 709
REFERENCE/DOCKET NUMBER: CSV-005.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
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Publication No. US20030180953A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
HAPPLICANT: Bo, Jiang
APPLICANT: Howard, Busone
APPLICANT: HOWARD Gene Disruption Methodologies for Drug Target Discovery
ITILE OF INVENTION NUMBER: US/10/032,585
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFFWARE: Patentin Version 3.1
SEQ ID NO 7296
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GREENER, TSVIKA,
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: REISS, YUVAL
APPLICANT: ALROY, IRIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
TITLE OF INVENTION: MATURATION
CURRENT APPLICATION NUMBER: 18/10/097,534
CURRENT PILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/204,24
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR PILING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-31
PRIOR PLING DATE: 2001-07-31
SPRIOR FILING DATE: 2001-107-31
SPRIOR FILING DATE: 2001-107-31
SPRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.3%; Score 92; DB 14; Length 832; Best Local Similarity 46.9%; Pred. No. 8.7e-07; Matches 15; Conservative 1; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                     TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10097534 Publication No. US20030049607A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Candida albicans
US-10-032-585-7296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-032-585-7296
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US-10-097-534-12
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Sequence 2167, Application US/10723860
; Sequence 2167, Application US/10723860
; Bublication No. US20040253606A1
; GENERAL INFORMATION:
    APPLICANT: Aziz, Natesha
; APPLICANT: Clinsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REPERENCE: 05882.0193.NPUSO1
; CURRENT APPLICATION NUMBER: US/10/723,860
; FILE REPERENCE: 05882.0193.NPUSO1
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2167
: LENGTH: 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
71.3%; Score 92; DB 16;
Best Local Similarity 51.6%; Pred. No. 9.1e-07;
Matches 16; Conservative 0; Mismatches 15;
                                                                                                                                                          Query Match 71.3%; Score 92; DB 14; Best Local Similarity 51.6%; Pred. No. 9.1e-07; Matches 16; Conservative 0; Mismatches 15.
                                                                                                                                                                                                                                                                                                                     331 PLPPGWEKRIDPRGRFÝYVDHNÍRÍTHVORP 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 PLPPGWEKRTDPRGRFYYVDHNTRTTTWQRP 361
                                                                                                                                                                                                                                                                    2 PLPXGWEXXXXXXXXXXYXXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: October 13, 2005, 14:49:59
ne : 71.3516 secs
SEQ ID NO 12
LENGTH: 870
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-723-860-2167
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-10-723-860-2167
                                                                                                           US-10-097-534-12
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5.1.6
Compugen Ltd.
GenCore version
Copyright. (c) 1993 - 2005
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- protein search, using sw model OM protein Run on:

October 13, 2005, 14:36:01; Search time 13.7802 Seconds (without alignments) 230.414 Million cell updates/sec

US-09-385-918-2 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

pir 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ubiquitin protein	ubiquitin-protein	ubiquitin-protein	ubiquitin-protein	probable ubiquitin	probable guanylate	yes-associated pro	45K WW domain-cont	45K WW domain-cont	ubiquitin-protein	hypothetical prote	synaptic scaffoldi	probable ubiquitin	protein F13E6.4 [i	NEDD-4 ORF - mouse	ubiquitin ligase N	hypothetical prote	brain-specific ang	yes-associated pro	eq	pr			peptidylprolyl iso	hypothetical prote	٦	hypothetical prote	ž	dystrophin, muscle
SUMMARIES	ΙD	58	10	T37545	_	T49744	~	B56954	JC7507	JC7508	T46412	T47801	T14152	T37900	G89632	183196	S70642	T23160	JE0209	A56954	150730	T46292	T33637	S68520	713	T02117	T25886	8	113	
	DB	7	Н	7	Н	7	7	~	~	7	~	~	7	~	~	N	~	7	7	N	~	~	~	N	~	~	N	~	N	П
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760	Query	72.1	71.3	71.3	71.3	71.3	70.5	69.8	67.4	67.4		_	62.9	65.1	64.3	64.3	64.3	62.8	62.0	61.2	æ	3	ч	45.3	45.3	43.8	43.4	42.6	42.6	42.6
	Score	93	92	92	92	92	91	90	87	87	87	86.5	85	84	83	83	83	81	80	79	75	68.5	99	æ	58.5	Ġ	26	52	52	25
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dystrophin - mouse	dystrophin, muscle	G-utrophin - mouse	utrophin - human	Pin1 protein homol	integrase-like pro	hypothetical prote	hypothetical prote	hypothetical prote	nuclear protein EM	hypothetical prote	beta-lactamase (EC	protein C43E11.3 [	formin binding pro	hypothetical Ww do	probable transcrip
\$28916	A27605	148373	528381	T08426	S22571	C70976	T49448	869038	T09579	T26779	JN0520	B87754	S64716	S58094	T08599
7	-	7	7	7	~	7	~	7	~	7	~	7	~	~	7
3678	3685	987	3433	166	499	158	234	465	397	120	311	1590	56	411	1098
42.6	42.6	40.3	40.3	39.9	39.9	39.5	37.6	37.2	36.8	36.4	34.9	34.9	34.1	34.1	34.1
52	55	52	52	51.5	51.5	51	48.5	48	47.5	47	45	45	44	44	44
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

```
Cispecies: Schizosaccharomyces pombe

Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

Cipatesion: T39585

Rivolckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

Submitted to the EMBL Data Library, August 1997

A; Reference number: 221865

A; Reference number: 221865

A; Recession: T39585

A; Recession: T39585

A; Recule Lype: DNA

A; Residues: 1-786 < VOLD-

A; Cross-references: UNIPROT: 014326; EMBL: Z99759; PIDN: CAB16903.1; GSPDB: GN00067; SPDB: SF

C; Genetics: A; Gene: SPDB: SPDC16E9.11c
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ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93; DB 2; Les
Pred. No. 1.8e-08;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 GRLPPGWERRADSLGRTYYVDHNTRTTTWTRP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: yeast ubiquitin-protein ligase;
F;236-273/Domain: Ww repeat homology <WRR1>
F;306-343/Domain: Ww repeat homology <WRR2>
F;364-401/Domain: Ww repeat homology <WWR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 16; Conservative
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A; Introns: 60/2
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ubiquitin-protein ligase (EC 6.3.2.19) - fission yeast (Schizosaccharomyces pombe)
NyAlternate names: E6-AP-like protein ubiquitin ligase
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004
C;Accession S66562; T45159
R;Nefsky, B.; Beach, D.
R;Nefsky, B.; Beach, D.
R;Nefsky, B.; Beach, D.
A;Title: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25
A;Reference number: S66562; MUID:96205868; PMID:8633463
A;Accession: S66562

A,Molecule type: mRNA A,Residues: 1-766 <NBF> A,Cross-references: UNTPROT:Q92462; GB:U66716; NID:g1519441; PIDN:AAB07514.1; PID:g15194 R,Nefsky, B.S.; Beach, D. submitted to the EMBL Data Library, August 1996 A,Description: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of

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A;Map position: 6
A;Introns: 11/1; 24/1; 59/2; 110/1; 783/2
C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.3%; Score 92; DB 1; 1
46.9%; Pred. No. 2.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: involved in endocytosis of GAP1 C; Superfamily: yeast ubiquitin-protein ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPLPXGWEXXXXXXXXXXXYXXHNTXTTXWXXP
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A.fene: SGD:RSP5, PUB1, NPI1, MIPS:YER125w
f.cross-references: MIPS:YER125w; SGD:S000927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;229-266/Domain: WW repeat homology <WW1>
F;331-368/Domain: WW repeat homology <WW2>
F;387-424/Domain: WW repeat homology <WW3>
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Matches 15; Conservative
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A, Residues: 1-101 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T49744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naturation protein ligame (EC 6.12.19) publ [validated] - fission yeast (Schizosaccharom N.Alternate names: ubiquitin ligame (EC 6.12.2.19) publ [validated] - fission yeast (Schizosaccharomyces pombe (S. Species: Schizosaccharomyces pomber: 1997)

A. Species: Schizosaccharomyces pombe (S. Species: Schizosaccharomyces)

A. Status; preliminary; translated from GB/EMBL/DDBJ

A. Status; preliminary; translated from GB/EMBL/DBJ

A. Status; preliminary; translated from GB/EMBL/GBJ

C. Status; pre
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A; Reference number: 222935
A; Accession: T45159
A; Accession: T45159
A; Accession: T45159
A; Cartus: prefilminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-766 «NE2>
A; Cross-references: EMBL:Y07592; PIDN:CAA68867.1
C; Genetics:
A; Gene: publ
C; Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
C; Keywords: ligase
F; 205-242/Domain: WW repeat homology «WW1>
F; 288-325/Domain: WW repeat homology «WW2>
F; 288-325/Domain: WW repeat homology «WW3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.3%;
46.9%;
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Best Local Similarity 46.55
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Matches 15; Conserv
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A;Molecule type: DNA
A;Residues: 1-809 <DIE>
A;Residues: 1-809 <DIE>
A;Cross-references: EMBL:U18916; NID:g1384128; PIDN:AAC03223.1; PID:g603364; GSPDB:GN000
R;Hein, C.; Springael, J.Y.; Volland, C.; Haguenauer-Tsapis, R.; Andre, B.
Mol. Microbiol. 18, 77-87, 1995
Mylitile: NPII, an essential yeast gene involved in induced degradation of Gapl and Fur4
A;Reference number: S70050; MUID:96154942; PMID:8596462
A;Accession: S70050
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C;Accession: T49744
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-809 <MUL>
A;Cross-references: UNIPROT:P39940; GB:U18916; EMBL:L11119; NID:g1384128; PIDN:AAC03223
ubiquitin-protein ligase (EC 6.3.2.19) RSP5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: E6-AP-like protein ubiquitin ligase; protein YER125w; PUB1 protein
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision
C;Accession: S43217; S50628; $70050
C;Accession: S43217; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, submitted to the EMBL Data Library, February 1993
A;Reference number: S30812
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;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, A:Reference number: S50628
A:Accession: S50628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ubiquitin-protein ligase [imported] - Neurospora crassa
NiAlternate names: protein 1824819.160
C.Species: Neurospora crassa
C.Species: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.160
A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 809;
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A;Cross-references: GB:AJ292969
C;Comment: This protein participates in a variety of cellular processes, such as proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8VEB2; GB:AJ292968
C;Comment: This protein participates in a variety of cellular processes, such as protein
during early developmental stage.
                                                                                                                                                                                                                                                       R;Valverde, P.
Biochem. Biophys. Res. Commun. 276, 990-998, 2000
A;Title: Cloning: expression, and mapping of hWW45, a novel human WW domain-containing
A;Reference number: JC7507; MUID:20483619; PMID:11027580
A;Accession: JC7507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rivalverde, P.
Biochem. Biophys. Res. Commun. 276, 990-998, 2000
Affile: Cloning, expression, and mapping of hWW45, a novel human WW domain-containing
A;Reference number: JC7507; MUID:20483619; PMID:11027580
A;Accession: JC7508
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NyAlternate names: hypothetical protein DKFZp434P2422.1
C;Species: Homo sapiens (man)
C;Accession: T46412
R;Blum, H; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
A;Reference number: Z23034
A;Accession: T46412
A;Status: preliminary
                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45K WW domain-containing protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 14q13-21, 14q21-23
C;Keywords: coiled coil: myristylation; protein degradation; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: ww45
C.Keywords: coiled coil; myristylation; protein degradation; transcription
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48.4%; Pred. No. 9.6e-08;
ative 0; Mismatches 16;
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Pred. No. 9.6e-08;
0; Mismatches 16;
         215 GPLPDGWEQAMTQDGEVYYINHKNKTTSWLDP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 PLPPGWSVDWTMRGRKYYIDHNTNTTHWSHP 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45K WW domain-containing protein - human
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Best Local Similarity 48.4%;
Matches 15; Conservative (
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Matches 15; Conservative
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A; Residues: 1-386 <VAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                               probable guanylate kinase (EC 2.7.4.8) 1, membrane-associated, splice form b - mouse C; Species: Mus musculus (house mouse)
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T42372
R; Dobrosotskaya, 1: Guy, R.K.; James, G.L.
J; Biol. Chem. 272, 31589-31597, 1997
A; Title: MAGI-1: a membrane-associated guanylate kinase with a unique arrangement of pro A; Title: MAGI-1: a membrane-associated guanylate kinase with a unique arrangement of pro A; Eference number: 222139; MUD:98058950; PMID:9395497
A; Accession: T42372
A; Molecule type: mRNA
A; Residues: 1-117 abobs
A; Conserved: all 11 abobs
A; Cross-references: UNIPROT:054893; EMBL:AF027503; NID:92702346; PID:92702347; PIDN:AAB9
A; Experimental source: strain C57 Black/6 x CBA
C; Genetics:
A; Genetics:
A; Genetics:
C; Keywords: alternative splicing; phosphotransferase
F; 340-337/Domain: WW repeat homology awwR2>
F; 347-384/Domain: WW repeat homology awwR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yes associated protein, 65k - mouse
N;Alternate names: YAP65 protein
C;Speciates: Mus musculua (house mouse)
C;Specias: Mus musculua (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: B56954; S46974
R;Sudol, M.; Bork, P.; Einbond, A.; Kastury, K.; Druck, T.; Negrini, M.; Huebner, K.; Le
J. Biol. Chem. 207, 14733-14741, 1995
A;Title: Characterization of the mammalian YAP (Yes-associated protein) gene and its rol
A;Recence number: A56954; MUID:95301570; PMID:778238
A;Status: preliminary
A;Receidus preliminary
A;Residues: 1-472 cSUD>
A;Cross-references: UNIPROT:P46938; EMBL:X80508; NID:9517178; PIDN:CAA56673.1; PID:95171
C;Genetics:
A;Gene: YAP65
C;Comment: This protein binds to the SH3 domain of the Yes proto-oncogene product.
C;Genetics:
A;Gene: YAP65
C;Superfamily: yes-associated protein; WW repeat homology
F;156-193/Domain: WW repeat homology cWW2>
F;215-252/Domain: WW repeat homology cWW2>
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                                                                                                                        Query Match 71.3%; Score 92; DB 2; Length 815; Best Local Similarity 46.9%; Pred. No. 2.8e-08; Matches 15; Conservative 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 472;
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46.9%; Pred. No. 3.5e-08;
iive 0; Mismatches 17; Indels
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Pred. No. 6.2e-08;
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F;239-276/Domain: WW repeat homology <WWR1>F;334-371/Domain: WW repeat homology <WWR2>F;393-430/Domain: WW repeat homology <WWR3>
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Best Local Similarity 46.9*
Matches 15; Conservative
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Best Local Similarity
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65.9%; Score 85; 45.2%; Pred. No.
  F;348-385/Domain: WW repeat homology <WWZ>
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                                                                                 Conservative
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                                                       Local Similarity
nes 14; Conserv
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-820 <AAA.
A;Cross-references: UNIPROT:Q9NT88; EMBL:AL137469
A;Experimental source: adult testis; clone DKFZp434P2422
C;Genetics: A;Genetics: A;Genetics: CDB:NEDD4
A;Ote: DKFZp434P2422.1
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
C;Keywords: ligase
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A;Introns: 7/1; 205/3; 250/1; 656/3; 713/3; 794/3; 964/3; 1232/3; 1298/3; 1445/3; 1523/3
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C;Genetics: A.SCAM
A,Gene: S.SCAM
A,Description: may assemble receptors and cell adhesion proteins at synaptic junctions
F;302-339/Domain: WW repeat homology <WW1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T47801

hypothetical protein F24G16.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47801
C;Accession: M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24477
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                                                                                                                                                                                                                                                                                           Length 820;
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1616 <DAN>
A,Cross-references: UNIPROT:Q9M127; EMBL:AL138647
A,Experimental source: cultivar Columbia; BAC clone F24G16
                                                                                                                                                                                    F;142-179/Domain: WW repeat homology <WWR1>
$132-379/Domain: WW repeat homology <WWR2>
F;393-430/Domain: WW repeat homology <WWR3>
F;489-814/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                       67.4%; Score 87; DB 2;
48.4%; Pred. No. 2.2e-07;
Live 0; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                  143 PLPPGWEEKVDNLGRTYYVNHNNRTTOWHRP 173
                                                                                                                                                                                                                                                                                                                                                                             2 PLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
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F;508-545/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                             Local Similarity 48.4 nes 15; Conservative
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A;Tille: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916 A;Note: see webbites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G89632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-671. ARIE-
A;Kesidues: 1-671. ARIE-
A;Cross-references: UNIPROT:09UTG2; EMBL:AL117390; PIDN:CAB55856.1; GSPDB:GN00066; SPDB:A;Experimental source: strain 972h-; cosmid c1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: UNIPROT:019404; GB:chr_X; PIDN:CAA92121.1; PID:93875841; GSPDB:GN000.
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                                                                                                                                                                                                                                                                                                                                                probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein F13E6.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, September 1999
A;Reference number: 221752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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DB 2; L
7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.1%; Score 84; DB 2; 43.8%; Pred. No. 5.9e-07;
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64.3%; Score 83; DB 2;
Best Local Similarity 41.9%; Pred. No. 5.9e-07;
Matches 13; Conservative 3; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: G89632
R,anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 GPLPAGWEMRLSEDYHVYFVDHSTKTTTWSDP 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
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                                                                                                                                                                                       303 PLPDNWEMAYTEKĠEVŸFIDHNTKTTSWLDP 333
                                                                                                                              2 PLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
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A,Introns: 60/2; 105/1; 639/2
F;242-279/Domain: WW repeat homology <WWR>
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NEDD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: 18196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Bjochem: Biophys Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression A;Reference number: 160167; MUID:92328780; PMID:1378265
A;Accession: 181196
A;Accession: 181196
A;Accession: 181196
A;Accession: 181196
A;Residues: I-708 <RES
A;Coss.references: GB:D10714; NID:9220508; PID:9220509
C;Genetics:
A;Genetics:
A;Gene
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Search completed: October 13, 2005, 15:11:14 Job time : 15.7802 secs

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09640 drosophila
094013 drosophila
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070466 anopheles g
092462 schizosacch
06641 debaryomyce
06690 neurospora
095xu3 caenorhabdi
097xv1 neurospora
075xu3 caenorhabdi
077v01 neurospora
075xu3 caenorhabdi
070v1 aschaya goss
06cn7 kluyveromyc
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06cn7 kluyveromyc
06cn7 kluyveromyc
06cn1 candida gla
06cc50 yarrowia 11
000308 homo sapien
09dbb0 mus musculu
08bzz3 mus musculu
07pqr2 anopheles g
06rhr9 mus musculu
08dbr1 homo sapien
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Q91w11
                                                                                                                                       1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                    1 GPLPXGWEXXXXXXXXXXXYXXHNTXTTXWXXPX 33
                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                       1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                            protein search, using sw model
                                                                                                         Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
                                                                    US-09-385-918-2
129
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		Q9h0m0 homo sapien	Q6dir6 xenopus tro	O42573 xenopus lae	Ofgmd5 xenopus lae	Q6h2y6 trypanosoma	Q9h4b6 homo sapien	Q6ia58 homo sapien	Q8veb2 mus musculu	Q8qgj2 gallus gall	Q9nt88 homo sapien	Q9h2w4 homo sapien	Q9bw58 homo sapien
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# ALIGNMENTS

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Q8IUY9 Q6P289 ITCH\_MOUSE

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366 GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDP 397

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                           SEQUENCE FROM N.A.

MEDLINE=22446065; PubMed=12537568;

Gelniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Patel S., Feiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.",
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whified E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.B., de Grey A.D., Drydale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 95; DB 2; Length 793; 50.0%; Pred. No. 2.6e-08; ive 1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subjected (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL; AE003523; AAS64973.1; -.
HSSP; P04410; 1A25.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                             a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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PROSITE; PS00499; C2_DOMAIN 1; UNKNOWN 1.
PROSITE; PS50004; C2_DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000008; Č2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR001599; HEGT.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PP001508; C2; 1.
Pfam; PP00632; HEGT; 1.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
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MEDINE-ZO19606; Pubbed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M. D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Richards S., Ambluner M., Henderson S.N., Brutcon G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Baltew R.M., Basu A., Baxendall G., Baytexterogiu L., Baldwin D., Rabeson K.Y., Banco P.V., Barnan B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bourler J., Baytexterogiu L., Bolshakov S., Botchan M.R., Botchan M.R., Buller R.M., Cawley S., Dahlke C., Davemport L.B., Davise P., M. Buttis K.C., Busam D.A., buller W. J., Brandari D., Bolshakov S., Buttler R., Dengelister C., Ferriaz C., Ferriaz C., Perriaz 
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                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Paclagas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                           Last annotation update)
                                                                                                                 Last sequence update)
                                                                                              Created)
                                                PRT;
                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 125-OCT-2004 (TrEMBLrel. 28, 12504682p (GG7555-PC).

Name=Nedd4; ORFNames=CG7555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                        Q95R64;
                                                095R64
RESULT 2
Q95R64
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.. 0

Gaps

.. 0

16; Conservative

Matches

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Local Similarity

(TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 26, Last annotation update)

Drosophilidae, Drosophila.

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STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AYOSB619; AAL13848.1; -.
                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0036736; Nedd4.
GO; GO:0016567; P:protein ubiquitination; NAS.
InterPro; IPR00569; HECT.
InterPro; IPR001202; WW Rsp5_WWP.
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PROSITE; PS01159; WW DOMAIN 1;
PROSITE; PS50020; WW DOMAIN 2;
SEQUENCE 838 AA; $6400 WW;
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Pfam, PF00397; WW, 3.
SMART, SM00119; HECTC; 1.
SMART, SM00456; WW, 3.
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                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                   Ephydroidea;
   01-DEC-2001
01-MAR-2004
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                                                                                                              MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
   Venter C.,
                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                      Lewis S.E., ^{\prime} "Annotation of the Drosophila melanogaster euchromatic genome: a
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vent Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 95; DB 2; Length 834;
Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMLARITY: Contains 1 C2 domain.
EMBL; AYOG153, AAL29143.1; -.
EMBL; AE003523; AAN11694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgm036736; Nedd4.
GO; GO:0016567; P:protein ubiquitination; NAS.
InterPro; IPR0000608; C2.
InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_RSP5_WWP.
Pfam; PF00159; HECT.
Pfam; PF00159; HECT; 1.
Pfam; PF00597; WW; 3.
                                                                                                                                                                                                                  Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50237; HECT; 1.
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PS50020; WW DOMAIN 2; 3.
834 AA; 95302 MW; CD
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50.0%;
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Best Local Similarity 50...
Best Local Similarity 50...
                                                                                                                                                                                                   genomics perspective.
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Gaps

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Score 95; DB 2; Length 838; Pred. No. 2.8e-08; 1; Mismatches 15; Indels

1 GPLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32

1;

16; Conservative

73.6%;

96400 MW; A3997EA6BB4A08D0 CRC64;

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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., A Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazel, R.G., Champe M., Pfeiffer B.D., A Man K.H., Doyle C., Baxerer E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., A Ballew R.M., Basu A., Baxendale J., Bayetkaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bennan B.D., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dudson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn P.,
                                                                                                                                          Name-Nedd4; ORFNames-CG755;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                     Last sequence update)
Last annotation update)
956 AA
                                                                                                                                                                                                                                        Ephydroidea, Drosophilidae, Drosophila
NCBI_TaxID=7227;
                                                 Created)
  PRT;
                                          01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
  PRELIMINARY;
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Gaps

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Indels

1; Mismatches

407 GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDP 438 

ò g 838 AA.

Q95TQ0 PRELIMINARY; PKI; Q95TQ0; 01-DEC-2001 (TrEMBLrel. 19, Created)

RESULT 3 Q95TQ0 ID Q95T AC Q95T DT 01-D

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Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Goldek A., Gong F., Garell J.H., Gu Z., Galbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M., Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wel M.H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McDerson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Puris D.L., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Sanders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Stapleton M., Stupski M.P., Smith T., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Zhan M., Zhang K., Zhan M., Zhang G., Zhao S., Wang S., Yao G., And Gibbs R.A., Myers E.W., Wenter J.C., The Gibbs R.A., Weissenbach J.C., The Gibbs R.A., Weissenbach J., The Gibbs R.A., Myers E.W., Weissenbach J., The Gibbs R.A., Weissenbach J., Weissenbach J., Zhan M., Zhang K., Zhan M., Zhang G., Zhao M., Weissenbach J., The Gibbs R.A., Myers E.W., Weissenbach J.C., The Gibbs R.A., Wyers E.W., Weissenbach J.C., Raith H.O., Raith G., Weissenbach J.C., Stapleton G. Drosophila melanogaster.", Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celliker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Savirskas R.A., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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EMBL, AR003523; AAN11695.1; -.
EMBL, OC2940; 1154.
FlyBase; FBgn0036736; Nedd4.
GO; CO:001657; P:procein ubiquitination; NAS.
InterPro; IPR00009; C2.
InterPro; IPR000973; C2_CalB.
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MEDLINE=22426065; PubMed=12537568;
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REDINE=20196006; Abbmed=10731132; DOI=10.1126/Science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., RA Baradon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D., Anti J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Baxendala G., Baytakraroglu L., Beasley E.M., Reeson K.Y., Benos P.V., Bennos P.V., Bandari D., Brottier P., Borkova D., Botchan M.R., Bouck J., Byrakraroglu L., Bessley E.M., Reeson K.Y., Dunn P., RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., R. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dunkov D., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Gersty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferras C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., Adlali M., Kalush F., Karpen G.H., Ke Z., Kanison J.A., Mostnefi A., Julalin, Kalush F., Karpen G.H., Ke Z., Kanison J.A., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattel B.E., Mattel B., Millon M. V., Mobarry C., Morris J., Moshrefi A., Mont S., Pollard J., Puri V., Pacleb J.M., Ralazzolo M., Pittman G.S., Pollard J., Puri V., Pacleb J.M., Shen H., Rhenert K., Remington K., Saunders R.D., Scheeler F., Shen H., Reinert K., Sanders R., Venter E., Shen H., Reinert K., Sanders R., Venter E., Shen H., Spier S
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG7555-PA (Putative ubiquitin ligase).
Name=Nedd4; Synonyms=DNedd4; ORFNames=CG7555;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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50.0%; Pred. No. 3.2e-08;
live 1; Mismatches 15;
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                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN 1.
PROSITE; PS5004; C2 DOMAIN 2; 1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS50129; WW DOMAIN 1; 3.
PROSITE; PS50120; WW DOMAIN 2; 3.
SEQUENCE 956 AA; 109543 WW; D42D3130C
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InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_Rsp5_WWP.
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Matches 16; Conservative
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                                                                             Pfam; PF00168; C2; 1.
Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
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Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
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"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stalleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL; AE003523; AAF49328.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myat A., McCabe V., Tear G.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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GO: GO: 1016567; P: procein ubiquitination; NAS.
InterPro: PR000009; CZ.
InterPro: IPR008973; CZ CalB.
InterPro: IPR008973; CZ CalB.
InterPro: IPR001202; WW_Rsp5_WWP.
Pfam; PF00168; CZ; 1.
Pfam; PF00397; WW; 3.
PRINTS; PR00397; WW; 3.
PRINTS; PR00397; WZ: 1.
SMART; SM00239; CZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                       MEDLINE=22426065; PubMed=12537568;
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se; FBgn0036736; Nedd4.
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STRAIN=9724;

WEDLINE=21848401; PubMed=11859360; DOI=10 1038/nature724;

WEDLINE=21848401; PubMed=11859360; DOI=10 1038/nature724;

WOOd V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squaros J., Peat N., Hayles J., Basham D., Bowamn S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Gonlies S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

A James K., Jones M., Squares R., Stevens K.,

A Nooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

A Jaylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Ber P., Zimmermann W., Britzc C., Holzer E., Moestl D., Hilbert H.,

Ber P., Zimmermann W., Wedler H., Wanbutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Golfeau A., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Shakovski G.V., Ussery D., Barrall B.G., Nurse P.;

When G. A., Weller M., Galllardin C., Taller P., Nurse P.;

When G. A., Weller M., Galllardin C., Nurse P.;

When G., Weller M., Gallardin C., Nurse P.;

When G., Weller M., Gallardin C., Nurse P.;

When G., Weller M., Gallardin C., Nurse P.;
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Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
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0
                                                                                                                                                                                                                                                                                                                                                                                     Length 1007;
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Schizosaccharomycetales; Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                73.6%; Score 95; DB 2; Le 50.0%; Pred. No. 3.3e-08; rative 1; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
E3 udditin-protein ligase pub3 (EC 6.3.2.-).
Mane-pub3; ORFNames-SPBC16E9.11c;
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDP 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   786 AA
SMART; SM00456; WW; 3.

PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN_1.

PROSITE; PS50004; C2_DOMAIN_2; 1.

PROSITE; PS5027; HECT; 1.

PROSITE; PS50020; WW_DOMAIN 1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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SEQUENCE
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Schizosaccharomyces.
NCBI_TaxID=4896;
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SEQUENCE
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubiquitin (By similarity).
FNAFYSGFVELVS -> LMHFILVLLNWYP (in Ref.
                                   SIMILARITY: Contains 1 C2 domain.
SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
PATHWAY: Ubiquitin conjugation; third step.
MISCELLANEOUS: A cysteine residue is required for ubiquitin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                 72.1%; Score 93; DB 1; Length 786; 50.0%; Pred. No. 5.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57B7A859F5497B9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 GRLPPGWERRADSLGRTYYVDHNTRTTTWTRP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GPLPXGWEXXXXXXXXXXYXXHNTXTTXWXXP 32
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                                                                             SIMILARITY: Contains 3 WW domains.
                                                                                                                                                                                                                                              HSSP; Q13526; IPIN.
GeneDB_SPombe; SPBC16E9.11c; -.
InterPro; IPR000008; C2.
InterPro; IPR008973; C2_CalB.
InterPro; IPR00569; WW.
InterPro; IPR002349; WW.
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WW 2.
WW 3.
HECT.
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Name=ENSANGG0000014008;
                                                                                                                                                                                                                      EMBL; AB001023; BAA19217.1; -. PIR; T39585; T39585.
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                                                                                                                                                                                                           EMBL; Z99759; CAB16903.1; -.
                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00403; WWDOMAIN.
                           thiolester formation.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                  domain.
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Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                      A GOS GO: 0005622; C:intracellular; IEA.

GO; GO: 0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO: 0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO: 0006512; P:ubiquitin cycle; IEA.

GO; GO: 0006512; P:ubiquitin cycle; IEA.

GO; GO: 0006512; P:ubiquitin cycle; IEA.

InterPro; IPR000089; C.2.

R InterPro; IPR00169; HECT.

R Pfam; PF00169; HECT; 1.

R Pfam; PF00163; HECT; 1.

R Pfam; PF00163; HECT; 1.

R PROSITE; PSS0037; WW A DOMAIN 2; 1.

R PROSITE; PSS0020; WW DOMAIN 1; 3.

R PROSITE; PSS0159; WW DOMAIN 1; 3.
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Trolerance of low ph in Schizosaccharomyces pombe requires
functioning publ ubiquitin ligase.";
Mol. Gene. 254:520-528(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 945;
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Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.1%; Score 93; DB 2; Le 51.6%; Pred. No. 7.1e-08; iive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        092462; 014454; 01-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) B3 ubiquitin--protein ligase publ (EC 6.3.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 PLPAGWEORRDPRGRVÝÝVDHNÍRÍTIWORP 424
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                                                                                                                                                              preliminary data.
EMBL; AAAB01008984; EAA14748.1; -.
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SEQUENCE FROM N.A.
MEDLINE=96205868; PubMed=8635463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 51.0...
-hes 16; Conservative .....xxx
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EMBO J. 15:1301-1312(1996)
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
A James K., Jones L., Jones M., Leather S., McDonald S., Jüdean J.,
A Money P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C.,
A Money P., Moule S., Mangall M.A., Rabbinowitsch E.,
A Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E.,
A Richerford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Relton J., Simmonds M., Squares R., Squares S., Stevens K.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmernann W., Wedler H., Wambutt R., Purnelle B.,
Coffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
Dominguez A., Revuelta J.L., Jümenez J., Sanchez M., del Rey F., Benito J.,
Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tamai K.K., Shimoda C.;

"The novel HECT-type ubiquitin-protein ligase Pub2p shares partially overlapping function with Publp in Schizosaccharomyces pombe.";

Gell Sci. 115:1847-1857(2002).

-!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates.

Regulates ubiquitination of cdc25.
-!- PATHWAY: Ubiquitination of cdc25.
-!- SUBCELLULAR LOCATION: Membrane-associated, and cytoplasmic.
-!- MISCELLANBOUS: A cysteine residue is required for ubiquitin-thiolester formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 C2 domain.
SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
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SMART; SM00239; C.2; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
PR0SITE; PS000499; C.2 DOMAIN 1; 1.
PR0SITE; PS500049; C.2 DOMAIN 2; 1.
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EWBL; 299161; CAB16867.1; --
EWBL; 299161; CAB16207.1; --
EWBL; 105795; AAB63350.1; --
PIR; S66562; S66562.

PIR; T37545; T37545.

PIR; T37545; T37645.

InterPro; IPR00009; C2.

InterPro; IPR00059; HECT.

InterPro; IPR001202; WW.

InterPro; IPR001202; WW.

PEAM; PP00168; C2; 1.

PEAM; PP00632; WW; 3.
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Dujon B., Sherman D., Fischer G., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Beisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Beisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Hantray F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
A Hantray F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
M., Mincker P., Souciet J.L.;
T., "Genome evolution in yeasts.";
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P39940 Saccharomyces cerevisiae Ubiquitin--protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames=DEHA0D04422g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Debaryomyces.
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                                                                    Conjugation, Ubl conjugation pathway.
                                                                                                   C2 domain...
WW 1...
Poly-Ala...
WW 2...
WW 3...
WW 3...
WW 3...
WW 6...
WM 9...
WB 6...
WB 6...
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WB 6...
WH 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.3%; Score 92; DB 1; I
46.9%; Pred. No. 8.8e-08;
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25-OCT-2004 (TrEMBLrel. 28, Last seq.
25-OCT-2004 (TrEMBLrel. 28, Last anno
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PROSITE; PS01159; WW DOMAIN 1; 3. PROSITE; PS50020; WW DOMAIN 2; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87267 MW;
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Matches 15, Conservative
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247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 AA;
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                                                                    Ligase; Repeat;
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294
351
463
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DOMAIN
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DOMAIN
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365 GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 396
                792 AA.
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                                                                                                                                                    PRELIMINARY;
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Submitted (OCT-2001)
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Submitted (NOV-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WormBase Consortium;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
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                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                      Gaps
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Neurospora genome project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Linsintarity: Contains 1.C2 domain.
EMBL, BX90812; Carefolf57.1, -..
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:lubjquitin-protein ligase activity; IEA.
GO; GO:0006812; P:ubjquitin-protein ligase activity; IEA.
InterPro; IPR0000893; C2.
InterPro; IPR000973; C2.
InterPro; IPR000569; HECT.
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46.9%; Pred. No. 9e-08;
tive 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                  Length 781;
                                                                                                                                                                                                        781 AA; 89368 MW; 98FA2CAAAFD92754 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 AA; 89265 MW; 14E9392E5AA3B923 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Probable ubiquitin-protein ligase.
                                                                                                                                                                                                                                            Query Match 71.3%; Score 92; DB 2; Best Local Similarity 46.9%; Pred. No. 8.9e-08; Matches 15; Conservative 1; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                             359 GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 390
                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0403; WWDOMAIN.
SMART; SM00239; C2; 1
SMART; SM00119; HECTC; 1.
SMART; SM00146; WW; 3.
PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS5004; C2_DOMAIN_2; 1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS501159; WW DOMAIN_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               787 AA
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          Pfam; PF0053; HECT; 1.
Pfam; PF00397; WW; 3.
SMART; SM00239; C2; 1.
SMART; SM0019; HECTC; 1.
SMART; SM00456; WW; 3.
PROSITE; PS50004; C2 DOWAIN_2; 1.
PROSITE; PS01159; WW DOWAIN_1; PROSITE; PS01159; WW DOWAIN_1; 3.
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InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PP00168; C2; 1.
Pfam; PP00532; HECT; 1.
Pfam; PP00397; WW; 3.
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Best Local Similarity 46.9
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
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                                                                                                                                                                                          Ligase.
SEQUENCE
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SEQUENCE
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
01-DEC-2001 (TrEMBLrel. 19, Created)
01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ww domain protein (E3 ubiquitin ligase) protein 1, isoform b.
Name=wwp-1; ORPNames=Y65B4BR.4;
Caenorhabditis elegans.
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STRAIN=Bristol N2;
Waterston R.;
Submitted (MOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maupin R., Bauer C.;
"The sequence of C. elegans cosmid Y65B4BR.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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WormBase; WBGene00007009; wwp-1.
WormPep; Y6584BR.4a; CE31384.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
 to the EMBL/GenBank/DDBJ databases.
                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                 Waterston R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR009973; C2 CalB.
InterPro; IPR001569; HECT.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00168; C2; 1.
Pfam; PF00632; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC024847; AAN73849.1;
HSSP; Q9HOMO; 1ND7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00397, WW, 4.
SMART, SM00239, C2, 1.
SMART, SM00119, HECTC, 1
                                   SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.H.;
Submitted (MAR-2000) t
 Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (MAY-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.;
Submitted (DEC-2003)
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WormBase Consortium;
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                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IntAct; Q9N2Z7;
                                                                                                                                                                        Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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"Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ww domain protein (E3 ubiquitin ligase) protein 1, isoform a.
Name=wwp-1; ORFNames=Y65B4BR.4;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                 MormBase; Various and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.3%; Score 92; DB 2; Length 792; Best Local Similarity 51.6%; Pred. No. 9.1e-08; Matches 16; Conservative 0; Mismatches 15; Indels
                                                       Waterston R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024847; AAN73850.1; -.
HSSE; Q9HOWO; 1ND7.
                                                                                                                                                Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90618 MW; D28EEDF864BAE1AC CRC64;
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STRAIN-Bristol N2;
Maupin R., Bauer C.;
"The sequence of C. elegans cosmid Y65B4BR.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 PLPQGWEMRRDPRGRVÝÝVDHNÍRÍTHVQRP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           792 AA;
                                     STRAIN-Bristol N2;
                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
                 EQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Q9N2Z7
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RESULT 14
RSP5_YEAST
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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
A Cui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.O., Jede G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
A Xarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
The Genome Sequence of the Fllamentous Fungus Neurospora crassa.",
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 0:0-0(2003).
-!- SIMILARITY: Contains 1 C2 domain.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                   Score 92; DB 2; Length 794;
Pred. No. 9.1e-08;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Probable ubiquitin--protein ligase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO.0005622; C:intracellular; IEA.
GO:0016874; F:ligase activity; IEA.
GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO:0006512; P:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00403; WWDOMAIN.
PROSTIE; PS50004; C2 DOMAIN.2; 1.
PROSTIE; PS01159; WW DOMAIN.1; 3.
PROSTIE; PS01020; WW DOMAIN.1; 3.
PROSTIE; PS00202; WW DOMAIN.2; 3.
HYPOCHELICAL protein; Ligams.
SEQUENCE 806 AA; 91484 MW; 5AAAAB41E51B38A CRC64;
                                                                                   794 AA; 90922 MW; 2080537AF4630BE5 CRC64;
                                                                                                                                                                                                                          254 PLPQGWEMRRDPRGRVYYVDHNTRTTTWQRP 284
                                                                                                                                                                                                                                                                                                                 806 AA.
                                                                                                                                                                                          2 PLPXGWEXXXXXXXXXXYYXXHNTXTTXWXXP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary data.
EMBL; AABX01000719; EAA28350.1; -.
HSSP; Q62940; 115H.
              PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002349; WW.
InterPro; IPR001202; WW_Rsp5_WWP.
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InterPro; IPR008973; C2 CalB.
InterPro; IPR000569; HECT.
                                                                                                                       71.3%;
51.6%;
                                                                                                        Query Match
Best Local Similarity 51.67
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
SMART; SM00456; WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=OR74A;
                                                                    Ligase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                 Q7RV01;
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                                                                                                                                                                                                                                                                                RESULT 13
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MEDLINE=96154942; PubMed=8596462;
Hein C., Springael J.-Y., Volland C., Haguenauer-Tsapis R., Andre B.;
"NPIJ, an essential yeast gene involved in induced degradation of Gapl
and Furt permeases, encodes the Rsp5 ubiquitin-protein ligase.";
Mol. Microbiol. 18:77-87(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6-
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIATE-2913264; PubMed-9169868; MEDIATE-913264; PubMed-9169868; MEDIATE-913264; PubMed-9169868; Araujo R., Aviles E., Berno A., Brennan T., Carpencer J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H. Lin D., Mosedale D., Nakhara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Bottsein D., Davis R.W.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95223981; PubMed=7708685; Huibregtse J.M., Scheffner M., Beaudenon S., Howley P.M.; Huibregtse J.M., Scheffner M., Beaudenon S., Howley P.M.; Affanily of proteins structurally and functionally related to the AP ubiquitin-protein ligase. "; Proc. Natl. Acad. Sci. U.S.A. 92:2563-2567 (1995).
                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                              .
0
                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin--protein ligase RSP5 (EC 6.3.2.-).
Name-RSP5, Synonyms-WNP1, NP11; OrderedLocusNames=YER125W;
ORFNames=SYGP-ORF41;
                 Length 806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howley P.M.;
                                              Indels
                DB 2; L
9.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95281634; PubMed=7761480;
Huibregtse J.M., Scheffner M., Beaudenon S., How
Proc. Natl. Acad. Sci. U.S.A. 92:5249-5249(1995)
                                                                                                           GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 415
                                                                             1 GPLPXGWEXXXXXXXXXXXYXXHNTXTTXWXXP 32
                                                                                                                                                                                      809 AA.
                                 Pred. No. 9.2e-
1; Mismatches
                   Score 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished observations (FEB-1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99077972; PubMed=9858558;
                 71.38;
46.98;
                                                Conservative
                                                                                                                                                                                      STANDARD;
Query Match
Best Local Similarity
. -hes 15; Conserve
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [6]
CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FY56;
                                                                                                                                                                                      YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Winston
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817 AA

PRT;

PRELIMINARY;

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Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 10895;
Voegell S.B., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
Philippsen P.,
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-- I SIMILARITY: Contains 1 C2 domain.
EMBL, AE016817; AAS51865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGD, ADLOSSC; -. Gintracellular, IEA. GO: 00005622; C: intracellular, IEA. GO: 0000542; F: ubiquitin-protein ligase activity, IEA. GO: GO: 0000512; P: ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGURY F PROJOCA WAS A W
                       Q75A12;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00008; C2.
InterPro; IPR00008; C2.
InterPro; IPR000973; C2 CalB.
InterPro; IPR000569; HECT.
InterPro; IPR001249; WW.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PP001568; C2: 1.
Pfam; PP000532; HECT; 1.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                 ORFNames=ADL055C;
                                                                                                                                                                                                                                                     NCBI_TaxID=33169;
                                                                                                                     ADL055Cp
     g
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ubiquitin.

L -> S (in RSPE-1; impaired in ubiquitin-
thioester formation and catalysis of
substrate ubiquitination).
C->A: Loss of ubiquitination.
6F1836384479E70F CRC64;
                 PATHWAY: Ubiquitin conjugation, third step.
SUBCELDULAR LOCATION: Cytoplasmic and nuclear (Potential).
SUBCELLULAR LOCATION: Cytoplasmic and nuclear (Potential).
INT. The ubiquitination appears to be the result of an INT. A cytoplasmic stansfer of ubiquitin.
MISCELLANEOUS: A cysteine residue is required for ubiquitin-thiolester formation.
SIMILARITY: Contains 1 C domain.
SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.3%; Score 92; DB 1; Length 809; 46.9%; Pred. No. 9.3e-08; ive 1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0000151; C:ubiquitin ligase complex; IDA.
GO; GO:00064842; F:ubiquitin-protein ligase activity; IDA.
GO; GO:0006313; P:chromatin assembly/disassembly; IMP.
GO; GO:0006513; P:protein monoubiquitination; IDA.
GO; GO:0000209; P:protein polyubiquitination; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSSUGGO; www.bornain.ci.j.
Ligase; Repeat; Ubl Conjugation pathway.
DOMAIN 229 262 domain.
DOMAIN 315 322 WW 1.
DOMAIN 315 322 Poly-Ala.
DOMAIN 387 420 WW 3.
DOMAIN 705 809 HECT.
                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 3 WW domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0403; WWDOMAIN.
SNART; SN00239; C2; 1.
SNART; SN00119; HECT; 1.
SNART; SN00456; WW; 3.
PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS50049; C2_DOMAIN_2; 1.
PROSITE; PS50137; HECT; 1.
PROSITE; PS50139; WW_DOMAIN_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR000008; C2.
InterPro; IRR0009973; C2 CalB.
InterPro; IRR0009973; C2 CalB.
InterPro; IRR000249; WW.
InterPro; IRR001202; WW.
Pfam; PRO10180; C2; 1.
Pfam; PRO0618; C2; 1.
Pfam; PRO06397; WW; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U18916; AAC03223.1; -. PIR; S43217; S43217.
HSSP; Q62940; 115H.
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nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IntAct; P39940; -. GermOnline; 139204; -. SGD; S000000927; RSP5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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 Length 817;
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71.3%; Score 92; DB 2; I
46.9%; Pred. No. 9.3e-08;
tive 1; Mismatches 16,
                                                                                                     395 GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 426
                                                                     Search completed: October 13, 2005, 15:09:15
Job time : 65.8571 secs
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es 15; Conservative
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387 GPLPSGWEMRLTNTARVYFVDHNTKTTTWDDP 418 

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Drosophil Human WW Yeast Rsp RSPS/9C p Yeast Rsp

AAR97683 AAB21979 AAB83022

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; Search time 85.6044 Seconds (without alignments) 171.684 Million cell updates/sec
                                                          218
1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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Compugen Ltd
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2105692 seqs, 386760381 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* geneseqp2003bs:\* Geneseg 16Dec04:\* geneseqp1980s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aab83018 Human Ned	Aae32726 Human NED	Adq07991 Human NED	Aay25170 Human KIA	Aae32725 Human NED	Aab83019 Human Ned	Adb49212 Mouse WW	Aar97680 Mouse Ned	Aab21978 Nedd4/mou	Adb49211 Human WW	Aaw13386 Human pro	Adq97134 Human can	Aau77715 Diseased	Abp58332 Human cel	Adb75453 Prostate	Adb75455 Prostate	Abg01080 Novel hum	Adr66480 Human pro	Adr66138 Human pro	Adg97130 Human can	Ado55161 Protein #	Adq97125 Mouse can	Adq07990 Human NED	Adq97128 Human can	Aaw93167 Human ZGG
ΙD	AAB83018	AAE32726	ADQ07991	AAY25170	AAE32725	AAB83019	ADB49212	AAR97680	AAB21978	ADB49211	AAW13386	ADQ97134	AAU77715	ABP58332	ADB75453	ADB75455	ABG01080	ADR66480	ADR66138	ADQ97130	ADO55161	ADQ97125	ADQ07990	ADQ97128	AAW93167
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% Query Match	100.0	100.0	100.0	100.0	100.0	95.9	95.9	93.1	93.1	93.1	67.9	67.9	6.79	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9	67.9
Score	218	218	218	218	218	209	209	203	203	203	148	148	148	148	148	148	148	148	148	148	148	148	148	148	148
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	ADB49213 Yeast WW				REMEMBEL 14
	7 ADB	5 AAU	4 AAE	6 AAE	
38 4	38			870	
9.09	9.09	58.9	58.9	58.9	
132	132	128.5	128.5	128.5	
41	42	43	44	45	

Human Nedd4 HECT E3 ubiquitin ligase WW domain #1. AAB83018 standard; peptide; 38 AA (first entry) 25-JUN-2001 AAB83018; AAB83018 

HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone encyhogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Nedd4. Human; HECT; homologous to E6 carboxyl terminus; ubiquitination;

Homo sapiens.

WO200116604-A1. 08-MAR-2001. 29-AUG-2000; 2000WO-US023729

99US-00385918. (SIGN-) SIGNAL PHARM INC. 30-AUG-1999;

Mercurio FM; Murray BW, Hoekstra MF, Xie W, WPI; 2001-327913/34.

Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.

Disclosure; Page 13; 75pp; English.

The present sequence is the ww domain of a HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase. The Ww domain binds to the Smad Py motif, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad Py motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein

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          bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated solutions are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; poliomyelitis; HIV; measles; protein therapy; human; NEDD4.
The method is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein complex comprising HECT-RCC1, viral maturation scaffolding protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles,
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                         Length 38;
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                                                                                                                                                                                                                                  1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                 SPLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQDNL 38
                                                                                                                                                                        100.0%; Score 218; DB 4;
100.0%; Pred. No. 2.3e-21;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by CAA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 16; 150pp; English
                                                                                                                                                                                                                                                                                                                                    AAE32726 standard; protein; 733
                                                                                                                                                                                                                                                                                                                                                                                                                      Human NEDD4 short form protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-2001; 2001US-0275224P.
31-JUL-2001; 2001US-0308958P.
07-DEC-2001; 2001US-0340170P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-2002; 2002WO-IB002106
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Greener T, Moskowitz H,
                                                                                                                                                                                       Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PROT-) PROTEOLOGICS LTD
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N-PSDB; AAD50460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 279
                                                                                                                                             Sequence 38 AA;
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The invention relates to a method for modulation of viral maturation. The invention also provides an isolated protein complex comprising a HECT-RCC1 selected from HETT-WW, HECT-RCC1, Gag protein, Gag late domain, Pl3, actin, myosin, Hsp60, Hsp70, Hsp90, STAM1, STAM2A, STAM2B, VHS-UIM, GTPase, E2 enzyme, teg101, cullin, HERC1, HRRC2, HERC3, Nedd4 -like protein or clathrin. The complexes, proteins, antibodies and methods are useful for treating viral infections, such as lymphosarcoma, human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides or nucleic acids for identifying a candidate beta-catenin pathway modulating agent or for modulating a beta-catenin pathway of a cell. The invention also relates to a method of modulating a beta-catenin pathway in a cell; and diagnosing a disease in a patient by detecting MBCAT expression. The invention is based on the finding that MBCAT orthologues are able to modify the beta-catenin pathway in Drosophila cells. Beta-catenin (also known as Armadillo in Drosophila) plays a role in cell signalling via the Wingless (Wg)/Wht signalling pathway which is involved in cell cycle progression. Beta-catenin levels are tightly regulated by a complex containing the tumour suppressor proteins APC (adenomatous polyposis coli) and Axin and the serine/threonine kinase GSK3-beta. In the absence of these proteins, beta-catenin accumulates in
immunodeficiency virus (HIV), hepatitis, poliomyelitis, measles, or Ebola and for inhibiting budding in a subject. They are also useful in diagnostic assays for determining whether a cell is infected with a virus and for characterising the nature, progression and/or infectivity of the infection. The invention is also useful in protein therapy. The present sequence is human NEDD4 protein used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a candidate beta-catenin MBCAT pathway modulating agent, useful for diagnosing and treating cancer, comprises providing an assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBCAT; modifier of beta-catenin; drug screening;
beta-catenin pathway modulator; Wingless signalling pathway;
Wg signalling pathway; cell cycle progression;
diagnosis; cancer; angiogenic disorder; appptotic disorder;
cell proliferation disorder; cytostatic; gene therapy; human; NBDD4;
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to the use of MBCAT (modifier of beta-catenin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neural precursor cell expressed developmentally downregulated
                                                                                                                                                                                                   Length 733;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for diagnosing and treating cancer, comprises pastem comprising a MBCAT polypeptide or nucleic acid
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                                                                                                                                                                                                                                                                                                   191 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 228
                                                                                                                                                                                                 Score 218; DB 6;
Pred. No. 6.5e-20;
; Mismatches 0;
                                                                                                                                                                                                                                                                                1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL
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                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NEDD4 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFSEQ; XM 046129.4.
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                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADQ07980
                                                                                                                                                              Sequence 733 AA;
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                                                                                                                            invention
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the nucleus where it acts as a transcriptional co-activator with TCF for the induction of target genes such as the cell-cycle regulators cyclin D1 and c-Myc. The Wingless/Deta-catenin signalling pathway is frequently mutated in human cancers, particularly those of the colon. Beta-catenin pathway modulating agents identified using the methods of the invention are useful as therapeutic agents for treating disorders associated with defective or impaired beta-catenin function and/or MBCAT function such as cancer, or angiogenic, apoptotic or cell proliferation disorders. Proteins that interact with MBCAT are also useful in detecting and providing information about the function of MBCAT proteins. The present sequence represents a human NED4 (neural precursor cell expressed, developmentally downregulated 4) protein, identified as an MBCAT polypeptide in an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitor; ubiquitin-mediated proteolyais; IkappaB polypeptide; HECT; ubiquitin-conjugating system; Homologous to E6-Ap carboxyl terminus; ligase; ubiquitini; ubiquitination; RSC ligase; KTAAN ligase; UBC4; MAD3; modulator; treatment; proliferative disorder; apoptosis; sepsis; differentiative disorder; viral infection; tissue wasting disorder; cachexia; malignancy; inflammatory disease; parasitic disease; tuberculosis; IL-2 therapy; rheumatoid strintiis; rheumatoid spondylitis; osteoarthritis; gouty arthritis; respiratory distress syndrome; cerebral malaria; chronic pulmonary inflammatory disease; silicosis; pulmonary sarcoidosis; bone resorption disease; reperfusion injury; graft versus host reaction; allograft rejection; Crohn's disease; systemic lupus erythematosus; leprosy; AIDS.
                                                                                                                                                                                                                                                                                                                                                             Gaps
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    32/
/note= "partial sequence, no start codon given"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-1999 (first entry)
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                Sequence 900 AA;
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comprises: (a) providing a ubiquitin-conjugating system infulbible of Ubiquitin-mediated proteolysis of a IkappaB polypeptide. The method comprises: (a) providing a ubiquitin-conjugating system including the IkappaB polypeptide and a HECT (Homologous to E6-Ap Carboxy) Terminus) comprises: (a) providing a ubiquitin-conjugating system including the ligase and ubiquitin, to promote ubiquitination of the IkappaB polypeptide by the HECT ligase; (b) contacting the ubiquitination of system with a candidate agent; (c) measuring a level of ubiquitination of the IkappaB polypeptide in the presence of the candidate agent in the presence of the candidate agent in the presence of the candidate agent is indicative of the IkappaB polypeptide in the absence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide of an inhibitor of ubiquitination of the IkappaB polypeptide of an inhibitor of ubiquitination of the IkappaB polypeptide of an inhibitor of ubiquitination of the candidate agent is indicative of an inhibitor of ubiquitination of the modulate spot of upidate agent is indicative of an inhibitor of upidate agent of a sasays can be used to identify compounds which modulators can be used e.g. in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, in the treatment of viral subtractors, and in the treatment of treatment of wiral whose interapy, rheumatory diseases, parasitic diseases, tuberculosis and high dose IL-2 therapy; rheumatory diseases, parasitic diseases, tuberculosis and chid mamatory diseases, silicosis, pulmonary sarchidosis, dronic pulmonary confittaneous, confitton, allografic or anumber of autoimmune diseases such as multiple solerosis, autoimmune diseases such as multiple solerosis, in the invention confit i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; poliomyelitis; HIV; measles; protein therapy; human; NEDD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                 This invention describes a novel assay identifying an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 927;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 255
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100.0%; Pred. No. 8.5e-20;
ive 0; Mismatches 0;
                    Disclosure; Page 68-71; 79pp; English.
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/note= "WW domain"
821. .923
/note= "HECT domain"
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Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 927 AA;
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Domain
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                                                                                                                                                                                                         The invention relates to a method for modulation of viral maturation. The invention also provides an isolated protein complex comprising a HECT-
GCI selected from HETT-WW, HECT-RCCI, Gag protein, Gag late domain, Pl3, actin, myosin, Hep60, Hsp70, Hsp90, STAMI, STAMZA, STAMZB, WS-UIM,
GTPASE, E2 enzyme, tsg101, cullin, HERCI, HERCI, HERCI, Nedd4 -like useful for treathing viral infections, such as lymphosarcoma, human immunodeficiency virus (HIV), hepatitis, poliomyelitis, measles, or Ebola and for inhibiting budding in a subject. They are also useful in and for characterising the nature, progression and/or infection with a virus and for characterising the nature, progression and/or infectivity of the infection. The invention is also useful in protein therapy. The present sequence is human NEDD4 protein used to illustrate the method of the
                                                                                                                            New protein complex comprising HECT-RCC1, viral maturation scaffolding protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles, or Ebola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HECT E3 ubiquitin ligame; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Nedd4.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; HECT; homologous to E6 carboxyl terminus; ubiquitination;
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100.0%; Pred. No. 8.5e-20;
ive 0; Mismatches 0;
                                                                      Alroy I;
                                                                      Reiss Y,
                                                                                                                                                                                        Disclosure; Fig 15; 150pp; English.
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           31-JUL-2001; 2001US-0308958P. 07-DEC-2001; 2001US-0340170P.
                                                                                                                                                                                                                                                                                                                                                                                                                            u similarity 100.0%;
38; Conservative 0
12-MAR-2001; 2001US-0275224P.
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                                              (PROT-) PROTEOLOGICS LTD
                                                                      Greener T, Moskowitz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SIGN-) SIGNAL PHARM INC.
                                                                                            WPI; 2003-111976/10.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                       N-PSDB; AAD50459
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 927 AA;
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The present sequence is the WW domain of a HECT (homologous to B6 carboxyl terminus) E3 ubiquitin ligase. The WW domain binds to the Smad PY the Saulting in ubiquitin ligase. The WW domain binds to the Smad PY the Saulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein the formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating that that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                           Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
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Pred. No. 3.6e-20;
0; Mismatches 1;
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   Mercurio FM;
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   Murray BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fowlkes DM;
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97.4%;
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97US-00826516.
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Hoekstra MF, Xie W,
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FOWLKES D M.
                                                                 WPI; 2001-327913/34
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Best Local Similarity
Matches 37; Conserv
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The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 681, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (I) with the certification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate antibodies. This is the amino condidates activities, or as an immunogen to generate antibodies. This is the amino condidates and demain.
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for discovering polypeptides or as an immunogen to generate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 38;
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Yes proto-oncogene associated protein; YAP; Nedd4.
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Pred. No. 3.6e-20;
0; Mismatches 1
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DELBRUECK CENT MOLECULAR MEDICINE MAX.
discovery, modification and refinement, involved in pharmacological activities,
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                                                                  5; 133pp; English
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Best Local Similarity 97.4%;
Matches 37; Conservative (
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95US-00476509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse Nedd4 WW domain-1.
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38 AA;
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(DELB-) DELBR
                                                                Example, Fig
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                                   antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR97680;
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identified in the Yes proto-oncogene associated proteins (YAPs) of consensus chicken, human and mouse (see also AAR97669-70 and AAR9762). A consensus sequence is given in AAR97671. Mouse Nedd4 plays a role in embryonic development and CNS differentiation. The Nedd4 WW domains (AAR97680-82) can be expressed in bacterial, yeast, insect or mammalian cells, and used to identify WW domain ligands. They can be introduced into cells, either directly or by gene therapy, to increase the level of signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW-domain; protein-protein interaction; cell growth regulation; protein degradation regulation; Alzheimer's; Dementia pugilistica; Down's syndrome; Parkinson's disease; Pick's; neurodegenerative; microtubule assembly; tau; hyperplasia; neoplasia; malignancy; psoriasis; retinosis; atherosclerosis; leukaemia; lymphoma; papiloma; pulmonary, fibrosis; rhematoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mediating protein-protein interactions, useful for regulating cell growth and for treating neurodegenerative disorders, comprises modulating binding of WW domain containing polypeptide with phosphorylated ligand.
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                              Length 38,
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                  1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                         1 SPLPPGWEERODVLGRTYYVNHESRRTOWKRPSPDDDL 38
                                                                                                                                                                                                            Score 203; DB 2;
Pred. No. 2.3e-19;
3; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nedd4/mouse peptide containing a WW-domain #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB21978 standard; peptide; 38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                              93.1%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscular dystrophy; mouse
                                                                                                                                                                                                                                                      34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 6; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-594014/56.
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou XZ;
                                                                                                                                                                       Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200048621-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999;
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Best Local
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21978
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Myotonic dystrophy, Niemann-Pick disease, prion disease with tangles, progressive supranuclear palsy and subacute sclerosing panencephalistis. In addition, inhibitors or stimmlators of interactions between WW-domains and ligands of the present invention can be used to treat hyperplastic and neoplastic disorders e.g. all forms of malignancies, psoriasis, retinosis, atherosclerosis resulting from plaque formation, leukaemias, benign tumour growth, lymphomas, papilomas, pulmonary fibrosis and rhematoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein; human; ned4; WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                             SPLPPGWEERQDVLGRTYYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                           Score 203; DB 3;
Pred. No. 2.3e-19;
                                                                                                                                                                                                                                                                                                        1 SPLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQDNL
                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human WW binding protein Ned4 WW domain #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 5; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00630916.
97US-00826516.
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                                                                                                                                                                                                                             93.1%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                34; Conservative
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FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-635075/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PIRO/) PIROZZI G.
(KAYB/) KAY B K.
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003077577-A1
                                                                                                                                                                                      Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-APR-1996;
03-APR-1997;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein ubiquitin ligases publ (AAW13384), pub2 (AAW13385) and pub3 (AAW13386) are homologues of fission yeast publ (AAW13387) and were identified from cDNA clones (AAT47040-42) obtd. e.g. from a keratinocyte CDNA library. Pub polypeptides can be produced in transfected host cells. They can control the steady state level of cdc25 phosphatese, the degree of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of p53). They can regulate cell or tissue differentiation, or cell growth or proliferation by affecting other proteins, can be a specific (ant)agonist of wild type protein function and may be used as immunogens to elicit a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Saccharomyces pombe protein ubiquitin ligase(s) - involved in phosphatase and p53 ubiquitination, and regulate cell growth and
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein ubiquitin ligase; pub2; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.
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                                                                                                                         Length 38;
                                                                                                                                                                             Indels
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1.4e-10;
7;
activities, or as an immunogen to generate antibod acid sequence of WW binding protein Ned4 WW domain
                                                                                                                                                                                                                                1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                         Score 203; DB 7; L. Pred. No. 2.3e-19; 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein ubiquitin ligase pub3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 87-91; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAW13386 standard; protein; 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US015930.
                                                                                                                         93.1%;
89.5%;
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                                                                                                                         Query Match
Best Local Similarity 89.5
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caligiuri M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-226206/20.
N-PSDB; AAT47042.
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nes 25, Conserv
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                                                                           Sequence 38 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-1996;
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gene therapy
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                                                               Sun H,
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                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                               New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating
                                                                                                                                                                                                                                                                                                                    The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kidney disease; nephrotropic; renal disease; IgA nephropathy; IgAN, asymptomatic microscopic haematuria; proteinuria; episodic gross haematuria; necrtishing crescentic glomerulonephritis; MCGN; minimal change disease; Min Ch; renal hypertrophy; diabetes; end-stage renal disease; ESRD; kidney function.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                          Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.
                                                                                                                                                                                                                                                                                                                                                                                                     Length 830;
                                                                                                                                                                                                                                                                                                                                                                                             Score 148; DB 8; Length 83:
Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diseased kidney tissue associated novel human protein #2.
                                                                         Human cancer associated sequence HP4-08-005, SEQ ID 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                            36
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD
                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 110; 199pp; English
                                                                                                                                                                                                                                                                               cancers such as leukemia and lymphoma
                AD097134 standard; protein; 830 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU77715 standard; protein; 834 AA
                                                                                                                                                                                                                                                                                                                                                                                                       67.9%;
                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                                  22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                     27-DEC-2002; 2002US-00330773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                          Morris DW, Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
.....hes 25; Conserva
                                                                                                                                                                                                                                            WPI; 2004-543781/52
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 830 AA;
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                                                                                                             Homo sapiens
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                                                      07-OCT-2004
                                                                                                                                                 22-JUL-2004.
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                                    ADQ97134;
RESULT 12
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compound libraries to discover movel therapeutics to regulate kidney function; as an antigen to raise polyclonal or monoclonal antibodies, and sa a therapeutic agent to rarget. Agents that modulate, up-or-down-regulate the expression of [11] or agents that agonise or antagonise the activity of the protein are useful to modulate biological and pathologic damage or end-stated with proteins function and activity, for e.g. kidney damage or end-stage renal disease (BSRD). This is the amino acid sequence of the diseased kidney associated novel human protein #2, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes an isolated nucleic acid molecule (I) that is expressed in diseased kidney tissue compared to normal kidney tissue. (I) and its encoded protein (II) are useful for diagnosing a renal disease state e.g. IgA nephropathy (IgAN) which presents as asymptomatic microscopic haematuria and/or proteinuria or episodic gross haematuria, merotosinging crescnitic glomerulonephritis (NCGN), minimal changed disease (Min Ch) or renal hypertrophy (the cause of end stage renal disease and early manifestation of diabetes), in a subject. (II) is useful: as a rarget for identifying agents which modulate the expression or activity of (I), for identifying binding partners, as novel target for screening synthetic small molecules and combinatorial or naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes that are differentially expressed in renal biopsy samples from patients with kidney diseases useful for diagnosing renal diseases such as IgA nephropathy or necrotizing crescentic glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 1.4e-10;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLPPGWEEKVDNLGRTYYVNHNNRTTOWHRPSLMD 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 62-65; 67pp; English
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71.4%;
03-AUG-2001; 2001WO-US024635
                                                                                                                            03-AUG-2000; 2000US-0222731P
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                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-257475/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
tes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      Munger WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABK11668
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New nucleic acid molecule, useful for diagnosing or treating prostate
                   Prostate; cancer; cytostatic; gene therapy; marker.
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                                                                                                                                                                                                                            25-JUL-2001, 2001US-0307982P.
22-ANG-2001, 2001US-0314356P.
25-SEP-2001, 2001US-032020P.
12-DEC-2001, 2001US-0341146F.
05-MAR-2002, 2002US-0362158P.
                                                                                                                                                                                      25-JUL-2002; 2002WO-US023913
                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-248033/24.
                                                                                                     WO2003009814-A2
                                                               Homo sapiens.
                                                                                                                                                                                                                         25-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel R,
                                                                                                                                               06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the protein sequence of human CGDD-3, a novel protein associated with cell growth, differentiation and death. The sequence is predicted from Incyte clone 366046cBL, which was isolated from a brain tumour tissue cell line CDNA library. Structural features catablish the protein as being associated with cell growth, differentiation and death, with further evidence suggesting it to be a differentiation protein ligase. The invention is based on novel human CGDD-1 to 21 proteins (see ABPS8330-50), the polynucleotides encoding them (see ABPS4689-709), and to the use of these for the diagnosis, treatment or prevention of cell proliferative disorders including cancer, cavelopmental disorders, neurological disorders, autoimmune disorders, reproductive disorders, and disorders of the placenta, and in the assessment of the effects of exogenous compounds on the activity and catherentiation and death
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Gandhi AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PG, Lee SY;
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human proteins associated with cell growth, differentiation and death, useful for treating, diagnosing or preventing cancer, developmental, neurological, reproductive or autoimmune/inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                       Azimzai Y, Au-Young JK, Batra S, Baughn MR, Becha SD;
Borowsky ML, Burford N, Ding L, Elliott VS, Emerling BM, Gai
Gietzen KJ, Griffin JA, Hafalla AJA, Honchell CD, Lal PG, L.
Lu DAM, Arvizu CS, Ramkumar J, Reddy R, Sanjanwala MM, Tang
Walia NK, Wang YE, Warren BA, Xu Y, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.9%; Score 148; DB 6; Length 854; 71.4%; Pred. No. 1.4e-10; ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 188-190; 238pp; English.
                                                                                                                                        06-APR-2001; 2001US-0282110P.
11-APR-2001; 2001US-0286820P.
27-APR-2001; 2001US-0286820P.
27-APR-2001; 2001US-028728P.
16-MAY-2001; 2001US-0291662P.
18-MAY-2001; 2001US-0291866P.
25-MAY-2001; 2001US-0293727P.
01-UUN-2001; 2001US-0295340P.
                                                                                                                                                                                                                                                                                                                                     15-JAN-2002; 2002US-0349705P
                                                                                                     05-APR-2002; 2002WO-US011152
                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-140453/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABZ24691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 854 AA;
                 WO200297032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zebarjadian Y;
                                                           05-DEC-2002
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Gorbatcheva Anderson D;

, Gannavarapu M, Glatt K, Zhao X,

Endege WO, Wonsey AM,

Monahan JE, Kamatkar S,

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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ABB5177-ABB7531 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at Etp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.9%; Score 148; DB 7; Lv
71.4%; Pred. No. 1.46-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PLPPGWEERQDILGRIYYVNHESRRIOWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 13, 2005, 15:00:31
Job time : 86.6044 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 854 AA;
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Gaps

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2 PLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQD 36

Best Local Similarity 71.4 Matches 25; Conservative

ð d ADB75453 standard; protein; 854 AA

RESULT 15 ADB75453 Prostate cancer marker protein.

(first entry)

04-DEC-2003

ADB75453;

BXXXXX

36, Appl 20, Appl 16857, A 21, Appl

37, Appl 19, Appl 7, Appli 12, Appl 12, Appl

Appl Appl App Appl

Sequence Sequence Sequence

12, Ap 2167,

Sequence

Sequence

Sequence

Sequence Sequence Sequence Sequence Seguence

31439, A 3, Appli 9, Appli

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Perfect score:

Run on:

Sequence:

Scoring table:

Database

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Sequence 3, Application US/10307956;
Sequence 3, Application US/10307956;
Publication No. US20030119072A1
GENERAL INFORMATION:
APPLICANT: Howekera, Merl F.
APPLICANT: Aie, Weilin
APPLICANT: Murray, Brion
FILE REFRENCE: 860098.433
CURRANT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/10/307,956
CURRANT FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 218; DB 14; Length 38; 100.0%; Pred. No. 9.1e-21; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
US-10-313-955-6
US-10-205-823-277
US-10-205-823-277
US-10-205-823-279
US-11-051-454-279
US-10-205-823-279
US-10-205-823-279
US-10-450-763-31439
US-10-450-763-31439
US-10-450-763-31439
US-10-707-534-9
US-10-205-823-275
US-10-205-823-275
US-10-105-050-30
US-10-105-050-30
US-10-105-050-30
US-10-105-050-30
US-10-105-050-30
US-10-105-050-30
US-10-640-361-12
US-10-640-361-12
US-10-640-361-12
US-10-640-361-12
US-10-640-361-12
US-10-105-050-36
US-10-105-050-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 38; Conservative
   ORGANISM: Homo sapien
   US-10-307-956-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Sequence 16, Sequence 18, Sequence 4, Sequence 36, Sequence 17, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

(cgn2 6/ptodata1/pubpaa/DCT_RW PUBCOMB.pep:*

(cgn2 6/ptodata1/pubpaa/DCT_RW PUB.pep:*

(cgn2 6/ptodata1/pubpaa/USO6 NEW PUB.pep:*

(cgn2 6/ptodata1/pubpaa/USO6 NEW PUB.pep:*

(cgn2 6/ptodata1/pubpaa/USO8 PUBCOMB.pep:*

(cgn2 6/ptodata1/pubpaa/USO8 NEW PUB.pep:*

(cgn2 6/ptodata1/pubpaa/USO8 PUBCOMB.pep:*

(cgn2 6/ptodata1/pubpaa/USO8 NEW PUB.pep:*

(cgn2 6/ptodata1/pubpaa/USO8 NEW PUB.pep:*
               5.1.6
Compugen Ltd
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US-10-097-534-16
US-10-097-534-15
US-10-185-050-18
US-10-307-956-4
US-10-185-056-36
US-10-185-056-36
US-10-687-361-11
US-10-644-631-11
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                1859788 segs, 416717961 residues
             GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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218
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Match
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RESULT

Sequence.

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Result Š.

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JS-10-185-050-18
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Publication No. US20030049607A1

GENERAL INFORMATION:

APPLICANT GREENER, TSVIKA

APPLICANT: REISS, YUVAL

APPLICANT: REISS, YUVAL

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL

TITLE OF INVENTION: MATURATION

FILE REFERENCE: PLV-001.01

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/275,224

PRIOR FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 71

SOSTWARE: PATCHTIN UNER: 201-12-07
                                                                                                            APPLICANT: MOSKOWITZ, ISVIKA
APPLICANT: REISS, YUVAL
TITLE OF INVENTION: CCMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
FILE REPREMENCE: PLV-001.01
CURRENT APPLICATION NUMBER: US/10/097,534
CURRENT PILING DATE: 2002-03-12
PRIOR PRILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
STOR APPLICATION NUMBER: 60/340,170
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 16
LENGTH: 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 218; DB 14; Length 733; Best Local Similarity 100.0%; Pred. No. 1.9e-19; Matches 38; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 218; DB 14; Length 927; 100.0%; Pred. No. 2.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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US-10-097-534-16; Application US/10097534; Sequence 16, Application US/10097631; Publication No. US20030049607A1; GENERAL INFORMATION: APPLICANT: GREENER, TSVIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-10-097-534-16
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ORGANISM: Homo sapiens
US-10-097-534-15
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Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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APPLICANT: Xie, Weilin
APPLICANT: Xie, Weilin
APPLICANT: Xie, Weilin
TITLEON: Brion
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 860098-431
CURRENT APPLICATION NUMBER: US/10/307,956
CURRENT FILING DATE: 2002-12-02
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: UNMBER: US/08/826,516
FILING DATE: 03-Apr-1997
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTONEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18 872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INDRER: 1101-208-999
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38;
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                                                                                                                                                                                                    NUMBER OF SEQUENCES: 213
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-185-050-18
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PRIOR FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
Sequence 18, Application US/10185050 Publication No. US20030077577A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10307956; Publication No. US20030119072A1; GENERAL INFORMATION:
                                                                           APPLICANT: Pirozzi, Gregorio
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STRANDEDNESS: <Unknown>
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Query Match
Best Local Similarity 97.47
Matches 37; Conservative
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Gaps
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                                                                                 ATORMEY/AGENT INCORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 789-9090
TELEFAX: (212) 789-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LEMCTH: 38 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10687361
; Publication No. US20040101896A1
; Publication No. US20040101896A1
; APPLICANT: Hunter, Tony
; APPLICANT: Lu, Kun Ping
; TITLE OF INVENTION: NIMA INTERACTING PROTEINS
; FILE REFERENCE: 66671-078
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 10/616,410
; PRIOR FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%; Score 203; DB 14
89.5%; Pred. No. 8e-19;
ative 3; Mismatches
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89.5%; Pred. No. 8e-19;
live 3; Mismatches
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Publication No. US20050027107A1
GENERAL. INFORMATION:
APPLICANT: Hunter, Tony
APPLICANT: Kun Ping, Lu
APPLICANT: Hanes, Steven D.
TILLE REFERENCE: 66671-085
FILE REFERENCE: 66671-085
CURRENT APPLICATION NUMBER: US/10/716,379
FILING DATE: 28-Jun-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-185-050-17
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Best Local Similarity 89.55
Matches 34; Conservative
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Best Local Similarity 89.5
Matches 34; Conservative
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US-10-687-361-11
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Publication No. US2003007757741
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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105-66-865-36
15 Squence 36, Application US/10256865
15 Publication No. US20030049672A1
15 GENERAL INFORMATION:
16 APPLICANT: Kun Ping Lu
17 TILE OF INVENTION: Methods and Compositions for Regulating
17 TILE OF INVENTION: Protein-Protein Interactions
17 TILE OF INVENTION: Protein-Protein Interactions
18 FILE REFERENCE: 140.1034-000
19 CURRENT APPLICATION NUMBER: US/10/256,865
19 PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/252,404
19 PRIOR FILING DATE: 1999-02-18
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                                                                                                                                                                                                                              1; Indels
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COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
                                                                                                                                                                                                                                                                                                    1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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                                                                                                                                                                               Score 209; DB 14;
Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 203; DB 14
Pred. No. 8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                            0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 38
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 233
                                                                                                                                                                             Query Match 95.9%;
Best Local Similarity 97.4%;
Matches 37; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%;
89.5%;
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                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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US-10-256-865-36
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ORGANISM:
                                              SEQ ID NO 4
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34; Conservative
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Best Local Similarity
Matches 25; Conserval
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                                                                                                                                               RESULT 12
US-10-313-955-6
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      Matches
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                                                                                                                                                                                                                              Length 38;
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                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                    1 SPLPPGWEERQDVLGRTYYVWHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                               1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                            93.1%; Score 203; DB 17;
89.5%; Pred. No. 8e-19;
tive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10648631

Bublication No. US20050049404A1

GENERAL INFORMATION:
APPLICANT: Hunter, Tony
TITLE OF INVENTION:
FILE REFERENCE: 66671-044

CURRENT APPLICATION NIMA INTERACTING PROTEINS
FILE REFERENCE: 66671-044

CURRENT APPLICATION NUMBER: US/10/648,631

CURRENT PILING DATE: 2003-08-25

PRIOR APPLICATION NUMBER: US/10/616,410

PRIOR APPLICATION NUMBER: US/10/616,410

PRIOR APPLICATION NUMBER: 2003-07-08

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 11

ERNOTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hunter, Tony
APPLICANT: Kun Ping, Lu
ITLE OF INVENTION: NIMA INTERACTING PROTEINS
FILE REFERENCE: 66671-043
CURRENT APPLICATION NUMBER: US/10/616,410
CURRENT PILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 09/275,900
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.1%; Score 203; DB 17
89.5%; Pred. No. 8e-19;
ive 3; Mismatches
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 10/616,410
PRIOR FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-10-616-410-11
Sequence 11, Application US/10616410
Publication No. US20050033032A1
GENERAL INFORMATION:
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89.5%;
                                                                                                                                                                                                                              Query Match 93.1
Best Local Similarity 89.5
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.5
Matches 34; Conservative
                                                                                                                                             TYPE: PRT
ORGANISM: Mus musculus
US-10-716-379-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus US-10-616-410-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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    Gaps
                                                                                                                                                                                                                                                                                              Caligiuri, Maureen
Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
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  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/313,955
FILING DATE: 05-Dec-2002
PRIOR APPLICATION DATA:
                                               1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                         1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.9%; Score 148; DB 14;
ilarity 71.4%; Pred. No. 2.5e-10;
Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/392,163
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: US 08/539,205
FILING DATE: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Post Office Square CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 277, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       Sequence 6, Application US/10313955; Publication No. US20030199036A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 834 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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AFFLICANI; ZEBRANALIZAN, FUGGINERI
FILE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
FILE REFERENCE: PI-0417 USA
CURRENT APPLICATION NUMBER: US/10/474,291
CURRENT APPLICATION NUMBER: US 60/349,705
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/349,705
PRIOR FILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/295,340
PRIOR APPLICATION NUMBER: US 60/295,340
PRIOR APPLICATION NUMBER: US 60/293,727
PRIOR APPLICATION NUMBER: US 60/293,727
PRIOR APPLICATION NUMBER: US 60/293,727
PRIOR APPLICATION NUMBER: US 60/291,846
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PRIOR APPLICATION NUMBER: US 60/291,846
PRIOR APPLICATION NUMBER: US 60/291,846
PRIOR APPLICATION NUMBER: US 60/291,662
PRIOR APPLICATION NUMBER: US 60/291,662
PRIOR PILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/286,820
PRIOR PILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/283,294
PRIOR PILING DATE: 2001-04-11
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 3660046CD1
US-10-287-218-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: AZIMAZAI, Yalda; AU-YOUNG, Janice K.
APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
APPLICANT: BECHA, Shanya D.; BONGWSKY, Mark L.
APPLICANT: BLIOTT, Vicki S.; EMERLING, Brooke M.
APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
APPLICANT: HOWCHELL, CYNTHA D.; LAL, Preeti G.
APPLICANT: HOWCHELL, CYNTHA D.; LAL, Preeti G.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: TANG, Y. Tom; CHAMLA, Narinder K.
APPLICANT: TANG, Y. Tom; CHAMLA, Narinder K.
APPLICANT: WANG, Yu-Mei B.; WARREN, Bridget A.
APPLICANT: YAO, MONIQUE G.; YUE, HENTY
APPLICANT: ZEBARADIAN, YEGANEN, MARTY
APPLICANT: ZEBARADIAN, YEGANEN, MARTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%; Score 148; DB 14; 71.4%; Pred. No. 2.6e-10; tive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/291,662
FILING DATE: 2001-05-16
APPLICATION NUMBER: US 60/287,228
FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10474291
Publication No. US20040132043A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
PRIOR
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APPLICANT: BATRA, Sajeev', BAUGHM, Mariah R.
APPLICANT: BATRA, Sajeev', BAUGHM, Mariah R.
APPLICANT: BATRA, Sajeev', BAUGHM, Mariah R.
APPLICANT: BUFORD, Neil; DING, Li
APPLICANT: BUFORD, Neil; DING, Li
APPLICANT: ELLOTT, Vicki S.; EMBRELING, Brooke M.
APPLICANT: GANDHI, Ameens R.; GIETZEN, Kimberly J.
APPLICANT: LEE, Soo Yeur; LU, Preeti G.
APPLICANT: HONCHELL, Cynthia D.; LaL, Preeti G.
APPLICANT: REDDY, Roopa; SANJANWALA, Madhu, M.
APPLICANT: TANG, Y. Tom, WALIA, Marinder K.
APPLICANT: TANG, Y. Tom, WALIA, Marinder K.
APPLICANT: TANG, Yu-mei, E.; WARREN, Bridget A.
APPLICANT: YO, Monique G.; YUE, Henry
APPLICANT: YO, Monique G.; YUE, Henry
APPLICANT: YO, Monique G.; YUE, Henry
APPLICANT: SEBRAJADIAN, Yeganeh
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
                                                                                                                                                                                                                  APPLICANT: Anderson, Dustin
TITLE OF INVENTION: MCFLORES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: MCFLORES FOR IDENTIFICATION, ASSESSMENT, PREVENTION, THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: MCFLORES FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
FRIOR APPLICATION NUMBER: 60/307,982
FRIOR FILING DATE: 2001-07-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-12-12
FRIOR FILING DATE: 2001-12-12
FRIOR FILING DATE: 2001-12-12
FRIOR FILING DATE: 2001-12-12
FRIOR FILING DATE: 2001-12-15
FRIOR FILING DATE: 2001-12-15
FRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SECTION NUMBER: 60/362,158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 148; DB 14;
Pred. No. 2.6e-10;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
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PRIOR FILING DATE: 2002-04-05
PRIOR PELLING DATE: 2002-04-05
PRIOR PELLING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 2001-06-01
PRIOR PLING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/287,218 CURRENT FILING DATE: 2002-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10287218 Publication No. US20030198975A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-205-823-277
                                                                                                                                                                                                     Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 277
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Search completed: October 13, 2005, 14:50:00 Job time : 82.011 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 13, 2005, 14:36:01; Search time 15.8681 Seconds (without alignments) 230.414 Million cell updates/sec Run on:

US-09-385-918-3 Title:

1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\*
pir2:\*
pir3:\* 4:64 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NEDD-4 ORF - mouse	ubiquitin ligase N	ubiquitin-protein	ubiquitin-protein	ubiquitin protein	probable ubiquitin	ubiquitin-protein	ubiquitin-protein	hypothetical prote	45K WW domain-cont	45K WW domain-cont	Pin1 protein - hum	peptidylprolyl iso	yes-associated pro	yes-associated pro	О	hypothetical prote	probable guanylate	brain-specific ang	yes-associated pro	ž	hypothetical prote	probable ubiquitin	Pinl protein homol	hypothetical prote	G	hypothetical prote	prote	protein F13E6.4 [i
SUMMARIES	DI	183196	S70642	T46412	843217	T39585	T49744	866562	T37545	T47801	JC7507	JC7508	868520	JC7136	B56954	150730	T14152	T46292	T42372	JE0209	A56954	S58094	T33637	T37900	T08426	588	S64713	T02117	T09579	963
	08	~	~	~	Н	~	~	-	7	N	0	0	N	~	N	N	~	~	~	~	N	~	~	N	~	N	7	0	7	~
	Length	708	887	820	809	786	815	,99	767	1616	383	386	163	165	472	448	1277	616	1111	1256	454	411	691	671	166	241	67	325	397	457
عان	Query Match	93	σ	67	9	5	Ŋ	S	26	53	45	2	44.7	4	4	4	39		38	37	37	36	m	36	36	35	n	4.	4.	ω.
	Score	203	199	148	132	130	130	123	123	115.5	86	96		97.5	91	88	87	83.5	83	82	81	80	80	79	78.5	78	77	75.5		74
	Result No.	1	7	m	4	ഗ	9	7	89	o,	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote protein C43E11.3 (	hypothetical prote	hypothetical prote	integrase-like pro	hypothetical prote	hypothetical prote	hypothetical prote	protein ZK1098.1 (	hypothetical prote	probable transcrip	formin binding pro	ATP-dependent DEAD	hypothetical prote	proteinase II VCA0
T19825	T20274 B87754	830014	T26779	S22571	T23160	869038	S40923	F88557	T49448	T08599	S64716	T52137	T46422	E82506
837 2	1590 2	583 2	120 2	499 2	1012 2	465 2	695 2	724 2	234 2	1098 2	26 2	619 2	1013 2	665 2
33.0	33.0	32.1	30.7	30.7	30.3	28.9	28.4	28.4	28.2	28.2	28.0	26.8	26.8	26.6
72	2 7	70	67	67	99	63	62	62	61.5	61.5	61	58.5	58.5	58
30	31 32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

```
C;Accession: 183196
R;Kunar, S.; Tomooka, Y.; Noda, M.
Biochem. Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression A;Reference number: 160167; MUID:92328780; PMID:1378265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: NEDD-4
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui C;Superfamily: ww repeat homology <WW2>
F;40.77/Domain: Ww repeat homology <WW2>
F;196-233/Domain: Ww repeat homology <WW3>
F;251-288/Domain: Ww repeat homology <WW3>
F;347-682/Domain: ww repeat homology <WW3>
F;347-682/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                            C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-708 <RES>
A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
                                                                                                                                                                                                                                                                         A;Accession: 183196
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.1.
Best Local Similarity 89.5'
Matches 34; Conservative
NEDD-4 ORF - mouse (fragment)
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1 SPLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQDNL 38 40 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 77 g ò

ubiquitin ligase Nedd4 - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

Cybace: 14 February Resquence\_revision 13 February Recor\_unange 03-001-2004

Ristaub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

Rystaub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

Rystaub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

Rystaub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

Rystatue: number: S70642

Ascentus: preliminary; nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 1-887 <STA>

A; Residues: 1-887 <STA>

C; Genetics:
C; Genetics:

A;Gene: Nedd4 Csuperfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui F;54-167/Domáin: protein kinase C C2 region homology <KC2> F;246-283/Domain: Ww repeat homology <WW1>

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A;Residues: 1-786 <VOL>
A;Cross-references: UNIPROT:014326; EMBL:299759; PIDN:CAB16903.1; GSPDB:GN00067; SPDB:SPR.
A;Experimental source: strain 972h-; cosmid c16E9
                                                                                                                                                                                                                                                                                                                                                                                          FUR4 protein; binds and ubiqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49744
                                                    A/Status: nucleic acid sequence not shown; not compared with conceptual translation A/Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable ubiquitin-protein ligase [imported] - Neurospora crassa
NiAlternate names: protein 1824819.160
C.Species: Neurospora crassa
C.Spacies: Q2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology FF:236-273/Domain: WW repeat homology < WWR1>F:366-343/Domain: WW repeat homology < WWR2>F:364-401/Domain: WW repeat homology < WWR2>F:364-401/Domain: WW repeat homology < WWR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Length 809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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C;Accession: T39585

S;VOlckaert, G; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitred to the EMBL Data Library, August 1997

A;Reference number: Z21865
A;Reference number: S70050; MUID:96154942; PMID:8596462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Accession: T39585
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.6%; Score 132; DB 1; Best Local Similarity 71.0%; Pred. No. 7e-09; Matches 22; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 LPPGWERRIDNFGRIYYVDHNTRITTWKRPT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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                                                                                                                                                      A, Residues: 1-101 <HEL>
C, Genetics:
A, Gene: SGD: RSP5, PUB1, NP11, MIPS: YER125w
A, Cross-references: MIPS: YER125w; SGD: S0000927
C, Function: SR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;331-368/Domain: WW repeat homology <WW2>F;387-424/Domain: WW repeat homology <WW3>
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Best Local Similarity 62.9°
Matches 22; Conservative
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A;Molecule type: DNA
A;Residues: 1-815 <SCH>
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                                            ;Accession: S70050
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A;Introns: 60/2
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Afane: ODB:NBDD4
A;Note: DKPZp414P2422.1
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
C;Keywords: ligase
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A Kesicule: type: DNA
A K. Cross-references: EMBL:U18916; NID:g1384128; PIDN:AAC03223.1; PID:g603364; GSPDB:GN006
A K. Cri. Springael, J. Y.; Volland, C.; Haguenauer-Tsapis, R.; Andre, B.
Mol. Microbiol. 18, 77-87, 1995
A Kritle: NP11, an essential yeast gene involved in induced degradation of Gapl and Fur4
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S562168: Saccharomyces cerevisiae

C; Species: Saccharomyces cerevisiae

C; Cate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C; Accession: S43217, S50628; S7050

S; Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Sthalingan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Sthalingan, J.T.; Dietrich, S43217

A; Reference number: S30812

A; Accession: S43217

A; Residues: 1-809 

A; Molecule type: DNA

A; Residues: 1-809 

A; Coresion: S43217

A; Residues: 1-809 

A; Corestion: February, December 1994

A; Residues: 1-809 

A; Residues: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ubiquitin-protein ligase (EC 6.3.2.19) NEDD4 - human (fragment)
NyAlternate names: hypothetical protein DKFZp434P2422.1
Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T464L2
Sylblum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                          Length 887;
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F;402-439/Domain: WW repeat homology <WW2>
F;459-496/Domain: WW repeat homology <WW3>
F;555-881/Domain: ubiquitin-protein ligase homology <UBI>
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F;342-379/Domain: WW repeat homology <WWR2>
F;393-430/Domain: WW repeat homology <WWR3>
F;489-814/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                              246 SPLPPGWEERQDVLGRTYYVNHESRTTQWKRPSPEDDL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T46412
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-820 AAA>
A;Cross-references: UNIPROT:Q9NT88; EMBL:AL137469
A;Experimental source: adult testis; clone DKF2p434P2422
                                                                                                                                                                                                                                                                                                                     1 SPLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.9%; Score 148; DB 2; L Larity 71.4%; Pred. No. 6.4e-11; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 PLPPGWEEKVDNLGRIYYVNHNNRTTQWHRPSLMD 177
                                                                                                                                                      Score 199; DB 2;
Pred. No. 2.1e-17;
4; Mismatches 1;
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                                                                                                                                                              91.3%;
86.8%;
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les 25; Conserv
                                                                                                                                                          Query Match
Best Local Similarity
Matches 33; Conserv
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A; Molecule type: DNA
A; Residues: 1-767 <MCL>
A; Residues: 1-767 <MCL>
A; Residues: 1-767 <MCL>
A; Cross-references: UNIPROT: Q92462; EMBL: Z99161; PIDN: CAB16207.1; GSPDB: GN00066; SPDB: SP
A; Experimental source: strain 972h-; cosmid 01167
B; Saleki, R.; Jáa, Z.; Karagiannis, J.; Young, P.G.
Mol. Gen. Genet. 254, 520-528, 1997
A; Title: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ ub
A; Reference number: Z07985; MUID: 97340937; PMID: 9197411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Description: involved in of the mitotic activating tyrosine phosphatase cdc25 [validat C, Function: arDL.

C, Function: arDL.

C, Function: arDL.

C, Superfamily: yeast ubiquitin-protein ligase; WW repeat homology

C, Keywords: cell cycle control; ligase

C, Keywords: cell cycle control; ligase

F, 206-242/Domain: WW repeat homology armus

F, 288-325/Domain: WW repeat homology armus

F, 382/Domain: WW repeat homology armus

F, 382/Domain: WW repeat homology armus
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A;Introns: 7/1; 205/3; 250/1; 656/3; 713/3; 794/3; 964/3; 1232/3; 1298/3; 1445/3; 1523/3
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A;Reference number: Z24477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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A;Experimental source: strain J227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F24G16.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 48.6%; Pred. No. 1.9e-06;
Matches 17; Conservative 9; Mismatches 8; Indels 1;
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A;Cross-references: UNIPROT:Q9M1Z7; EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB 2; L
Pred. No. 9.4e-08;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APLPPGWEKRADAVTGKSYYIDHNTKTTTWSHPCP 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: EC 6.3.2.19 [validated, MUID:96205868] C; Function: <CYC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SPLPPGWEERQD-ILGRIYYVNHESRRIQWKRPTP 34
                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <SAL>
        preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 LPPGWERRTDNLGRTYYVDHNTRSTTWIRP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LPPGWEERQDILGRIYYVNHESRRTQWKRP
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45K WW domain-containing protein - human
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Best Local Similarity 70.0°
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: publ; SPDB:SPAC11G7.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Map position: 1
A, Introns: 6/2; 14/1; 62/2
C, Function: <UBI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T47801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T47801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: F24G16.40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
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NiAlternate names: BC-AP-like protein ubiquitin ligase
C; Species: Schizosaccharomyces pombe
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C; Accession: $66562; T45159
R; Neffsky, B.; Baach, D.
EMBO J. 15, 1301-1312, 1996
A; Title: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25
A; Recence number: $66562; MUID: 96205868; PMID: 8635463
A; Accession: $66562; MUID: 96205868; PMID: 96306716; NID: 91519443; PIDN: AAB07514.1; PID: 915194
A; Residues: 1-766 *ANEP-
A; Cross-references: UNIPROT: Q92462; GB: U66716; NID: 91519443; PIDN: AAB07514.1; PID: 915194
A; Residues: Lothe EMBL Data Library, August 1996
A; Description: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of A; Argerence number: 222935
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Widgutin-protein ligase (EC 6.3.2.19) publ [validated] - fission yeast (Schizosaccharom NyAlternate names: ubiquitin ligase Publ
C;Species: Schizosaccharomyces pombe
C;Species: 30-loc-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37545; T48655
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A;Reference number: Z21722
A;Accession: T37545
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A;Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.160
C;Genetics:
A;Gene: NCSP:B24B19.160
A;Map position:
C;Superfamily: 24/1; 59/2; 110/1; 783/2
C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology F;334-371/Domain: WW repeat homology <WWR1>F;33-371/Domain: WW repeat homology <WWR2>F;334-371/Domain: WW repeat homology <WWR2>F;334-371/Domain: WW repeat homology <WWR2>F;334-371/Domain: WW repeat homology <WWR3>F;393-430/Domain: WW repeat homology <WWR3>F;393-430/Domain: WW repeat homology <WWR3>F;394-371/Domain: WW Repeat homology <WWR3>F;394-371/DOMAIN:
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C;Genetics:
A;Gene: publ
C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
C;Keywords: ligase
E;205-242/Domain: WW repeat homology < WW1>
F;288-325/Domain: WW repeat homology < WW2>
F;345-382/Domain: WW repeat homology < WW3>
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1 Similarity 70.0%; Pred. No. 9.4e-08;
21; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130; DB 2;
Pred. No. 1.3e-08;
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A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 59.6%;
1 Similarity 71.0%;
22; Conservative 5
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Best Local Similarity
Matches 22; Conserv
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Best Local S
Matches 21
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Gaps

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Indels

Length 163;

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C;Accession: JC7136
R;Fujimori, F.; Takahashi, K.; Uchida, C.; Uchida, T.
Biochem. Biophys. Res. Commun. 265, 659-663, 1999
A;Title: Mice lacking Pini develop normally, but are defective in entering cell cycle fr. A;Reference number: JC7136; MUID:20070807; PMID:10600477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-165 <FUJ>
A;Residues: 1-165 <FUJ>
A;Cross-references: UNIPNOT:Q9QUR7; DDBJ:AB009691; NID:g6468199; PIDN:BAA87037.1; PID:g6.
C;Comment: This protein is a member of peptidyl prolyl cis/trans isomerase family. It is tes in oligopeptides, controls G2/M transition of HeLa cells, regulates entry into G1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C,Accession: B56954; S46974
R;Sudol, M.; Bork, P.; Einbond, A.; Kastury, K.; Druck, T.; Negrini, M.; Huebner, K.; Lel
J. Biol. Chem. 270, 14733-14741, 1995
A;Title: Characterization of the mammalian YAP (Yes-associated protein) gene and its rol.
A;Reference number: A56954; MUID:95301570; PMID:7782338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidylprolyl isomerase (EC 5.2.1.8) - mouse
NiAlternate names: parvulins, Pinl protein
C:Species: Mus musculus (house mouse)
C:Species: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat homology
                                                                                                                          Score 97.5; DB 2;
Pred. No. 3.3e-05;
5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 97.5; DB 2;
Pred. No. 3.3e-05;
5; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: yeast ESS1 protein; WW repeat homology C;Keywords: cis-trans-isomerase; mitosis F;5-43/Domain: WW repeat homology <WWR>
                C,Superfamily: yeast ESS1 protein; WW repeat homology
F;5-43/Domain: WW repeat homology <WW1>
                                                                                                                                                                                                                                                                                             3 LPPGWEERQD-ILGRTYYVNHESRRTQWKRPT 33
                                                                                                                                                                                                                                                                                                                                          LPPGWEKRMSRSSGRVYYFNHITNASQWERPS 38
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F,156-193/Domain: WW repeat homology <WW1>
F,215-252/Domain: WW repeat homology <WW2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yes-associated protein, 65k - mouse N;Alternate names: YAP65 protein C;Species: Mus musculus (house mouse)
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Best Local Similarity 53.1%;
Matches 17; Conservative
                                                                                                                                  44.78;
                                                                                                                                                                       Best Local Similarity 53.1%;
Matches 17; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                  Query Match
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C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7507
C;Accession: JC7507
B;Valverde, P.
Biochem. Biophys. Res. Commun. 276, 990-998, 2000
A;Title: Cloning, expression, and mapping of hWW45, a novel human WW domain-containing G A;Reference number: JC7507; MUID:20483619; PMID:11027580
A;Accession: JC7507
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-383 <VAL>
A;Residues: 1-383 <VAL>
A;Cross-references: GB:AJ292969
C;Comment: This protein participates in a variety of cellular processes, such as protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8VEB2; GB:AJ292968
C;Comment: This protein participates in a variety of cellular processes, such as protein
during early developmental stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-163 <LUK>
A;Cross-references: UNIPROT:Q13526; EMBL:U49070; NID:g1332709; PIDN:AAC50492.1; PID:g133
C;Genetics:
A;Gene: GDB:PIN1; dod
A;Cross-references: GDB:5218381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45K WW domain-containing protein - mouse

6.Species: Mus musculus (house mouse)

C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004

C.Accession: UC7508

B.Valverde, P.

B.Valverde, P.

B.Yaltle: Cloning, expression, and mapping of hWW45, a novel human WW domain-containing A;Reference number: UC7507; MUID:20483619; PMID:11027580

A;Reference number: MUID:20483619; PMID:11027580

A;Ression: UC7508

A;Ressidues: 1-386 <VAL>
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Pinl protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accesion: S6850
C;Accesion: S6850
R;Lu, K.P.; Hantes, S.D.; Hunter, T.
Nature 380, 544-547, 1996
A;Ttle: A human peptidyl-prolyl isomerase essential for regulation of mitosis.
A;Reference number: S68520; MUID:96195064; PMID:8606777
A;Reference number: S68520; MUID:96195064; PMID:9606777
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A;Gene: ww45
C;Keywords: coiled coil; myristylation; protein degradation; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 14q13-21, 14q21-23
C;Keywords: coiled coil; myristylation; protein degradation; transcription
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Pred. No. 7.1e-05;
6; Mismatches 16
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ilarity 40.5%;
Conservative
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Best Local S
Matches 15
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A;Gene: ww45
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Gaps

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Indels

Length 165;

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Gaps

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Indels

Length 472;

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RESULT 15
150730
yes-associated protein, 65K - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: 150730; S39260
R;Sudol, M.
Oncogene 9, 2145-2152, 1994
A;Title: Yes-associated protein (YAP65) is a proline-rich phosphoprotein that binds to the A;Reference number: 150730; MUID:94309887; PMID:8035999
A;Accession: 150730
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gesidues: 1.448 cSUD>
A;Gesidues: UNIPROT:P46936; EMBL:X76483; NID:9434017; PIDN:CAA54021.1; PID:94340
C;Genetics:
A;Gene: YAP65
C;Superfamily: yes-associated protein; WW repeat homology
F;169-206/Domain: WW repeat homology < WW1>
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216 PLPDGWEQAMTQDGEVYYINHKNKTTSWLDP 246
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Search completed: October 13, 2005, 15:11:14 Job time : 15.8681 secs

170 PLPPGWEMAKTPSGQRYFLNHIDQTTTWQDP 200

8 8

THE PACE OF THE PA

us-09-385-918-3.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 13, 2005, 14:03:23 ; Search time 72.381

on: October 13, 2005, 14:03:23; Search time 72.381 Seconds (without alignments) 268.842 Million cell updates/sec

Title: US-09-385-918-3
Perfect score: 218
Sequence: 1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38

Sequence: 1 SPLPPGWEERQDILGRIYYVNH Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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tion	homo sapien	oryctolagus	mus musculu	rattus norv	mus musculu	homo sapien	mus musculu	homo sapien	homo sapien	mus musculu	mus musculu	mus musculu	homo sapien	gallus gall	xenopus tro	xenopus lae	xenopus lae	anopheles g	drosophila	drosophila	drosophila	drosophila	drosophila	anopheles g	saccharomyc	ashbya goss					
Description	P46934	Q9n134	P46935	062940	Q80u03	Q9nt88	Q8brt9	Q9h2w4	Q9bw58	Q99pk2	Q8cfi0	Q641n8	Q8n5a7	Q7z5£1	Q96pu5	Q7z5£2	Q725n3	043165	. Q8qgj2	Q6dir6	042573	Qegmd5	07qe76	Q7kur2	Q95r64	Q95tg0	Q8igr6	Q9vvi3	Q7pqr5	P39940	Q75ai2
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ID	NED4 HUMAN	Q9N134	NED4_MOUSE	NED4_RAT	080003	Q9NT88	Q8BRT9	Q9H2W4	Q9BW58	Q99PK2	QBCFIO	Q641NB	Q8N5A7	Q725F1	Q96PUS	Q725F2	Q7Z5N3	043165	Q8QGJ2	Q6DIR6	042573	Q6GMD5	Q7QE76	Q7KUR2	Q95R64	Q95TQ0	Q8IQR6	Q9VVI3	Q7PQR5	RSP5_YEAST	Q75A <u>T</u> 2
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% Query Match	100.0	7.76		91.3	67.9	67.9	6.79	67.9	67.9	67.9	67.9	67.9	67.9			٠.	٠.	67.9	99	65.6	65.1	S	63.8	63.3	٠.	•	63.3	63.3	61.9	9.09	9.09
Score	218	213	203	199	148	148	148	148	148	148	148	148	148	148	148	148	148	148	145	143	142	142	139	138	138	138	138	138	135	132	132
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Q6cnc7 kluyveromyc Q6fn71 candida gla Q6bt11 debaryomyce Q14126 schizosacch Q6m906 neurospora Q7rv01 neurospora Q0308 homo sapien Q9cb0 mus musculu Q6c289 mus musculu Q9c9070 mus culu Q9c9070 mus culu Q9c9070 musculu Q9c908 sus musculu Q9c102 homo sapien Q8c2c3 mus culu Q9c102 komo sapien Q8c2c3 sus susculu Q9c102 schizosacch
Q6CNC7 Q6FN71 Q6FN71 Q6BT41 PUB3 SCHPO Q6M906 Q7RV01 WWP2 HUMAN WWP2 HUMAN WWP2 HOUSE ITCH MOUSE ITCH HUMAN WWP1 MOUSE ITCH HUMAN
ппоннинивния
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132 132 131 130 130 128.5 128.5 128.1 128.1 128 128
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## ALIGNMENTS

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 25, Last sequence update)
Ubiquitin-procein ligase Nedd4 (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.20'; ww_DOWALL_2'; 4.

1 Ubl conjugation; Ubl conjugation pathway.

9 44 Pro-rich.

77 81 Poly-Ser.

85 288 Poly-Gin.

91 324 WW 1.

48 481 WW 2.

554 WW 4.

65 1000 HECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functional sodium channel.";
Mm. J. Physiol. Renal Physiol. 280:F530-F539(2001).
EMBL; AF229024; AAF45194.1; -.
HSSP; Q62940; 115H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 218; DB 1; 100.0%; Pred. No. 7.8e-20;
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InterPro; IPR008973; C2 Calb.
InterPro; IPR001202; WW_Rsp5_WWP.
                                                                                                   InterPro; IPR000008; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR008973; C2 CalB.
InterPro; IPR000569; HEGT.
InterPro; IPR001202; WW_Rep5_WWP.
Pfam; PF00168; C2; 1.
Pfam; PF001397; WW; 4.
PRINTS; PR00360; C2D0NAIN.
SWART; SM00119; HEGT; 1.
SWART; SM00119; HEGT; 1.
SWART; SM00456; WW; 4.
PROSITE; PS50049; C2_DOMAIN_2; 1.
PROSITE; PS5004; C2_DOMAIN_2; 1.
PROSITE; PS50019; WW_DOMAIN_2; 1.
PROSITE; PS50019; WW_DOMAIN_2; 1.
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SMART; SM00456; WW; 4.
PROSITE; PS01159; WW_DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
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Matches 38; Conservative
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                 Genew; HGNC:7727; NEDD4.
H-InvDB; HIX0012269; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=9228780; PubMed=1378265; Kumar S., Tomooka Y., Noda M.; Kumar S., Tomooka Y., Noda M.; "Identification of a set of genes with developmentally down-regulated expression in the mouse brain."; Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION, AND INTERACTION WITH UBE2D2
                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hatakeyama S., Jensen J.P., Weissman A.M.; "Subcellular localization and ubiquitin-conjugating enzyme (E2) interactions of mammalian HECT family ubiquitin protein ligases."; J. Biol. Chem. 272:15085-15092(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6 X CBA;
MEDLINE=97326076; PubMed=9182527; DOI=10.1074/jbc.272.24.15085;
                                                                          Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
MEDLINE=22354683; PubMed=12466851; Adaphi I Rono H. Kon
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kumar S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
51811 MW; D1C4549B52E22298 CRC64;
                                                                                                                                                                                                                                                                                                              SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDSL 135
                                                                               Score 213; DB 2; L
Pred. No. 1.5e-19;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAG255, 008758; QBBGB3; OLOCT-2003 (Rel. 32, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin-protein ligase Nedd-4 (EC 6.3.2.-).
Name=Nedd4; Synonyms=Kiaa0093, Nedd-4, Nedd4a;
                                                                                                                                                                                                                                                               1 SPLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       887 AA
                                                                                                                                                                       1; Mismatches
                                                                                   97.78;
97.48;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                     Query Match
Best Local Similarity
Thes 37; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
455 AA;
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Rotin D.
  DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakajima D., Nagase T., Ohara O., Koga H.;
"Prediction of the conding sequences of mouse homologues of KIAA gene:
"Prediction of the conding sequences of 400 mouse KIAA-homologous
connected an unclocide sequences of 400 mouse KIAA-homologous
connected an acception of terminal sequences of connected connected parampled from size-fractionated libraries.";

NAR Seas. 10:35-48(2003).

-!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates (By
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- TISSUE SPECIFICITY: Brain.
-i- MISCELLANBOUS: A cysteine residue is required for ubiquitin-
thiolester formation: (?) Anmain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Involved in the embryonic development and differentiation of the central nervous system. PATHWAY: Updquitin conjugation; third step. SUBUNIT: Binds SCNNIA, SCNNIB and SCNNIG (By similarity) interacts with UBE2D2. SUBCELLULAR LOCATION: Cytoplasmic. TISSUE SPECIFICITY: Brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 3 WW domains.
CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005829; C:cytosol, IDA.
GO:000151; C:ubiquitin ligase complex; IPI.
GO:0005815; Piprotein binding; IPI.
GO:0004842; F:ubiquitin-protein ligase activity; IDA.
erPro; IPR000008; C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligame, Repeat, Ubl ConjugaTion, Ubl conjugation pathway. DOMAIN 65 166 C2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U96635; AAB63360.1; ALT_FRAME.
AK088620; BAC40458.1; --
AK088767; BAC40558.1; --
AK122203; BAC65485.1; --
Q62940; 115H.
                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=22579291; PubMed=12693553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00499; C2_DOMAIN_1; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50207; HECT; 1.
PROSITE; PS01159; WW_DOMAIN 1; 3.
PROSITE; PS50020; WW_DOMAIN_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000008; C2.
InterPro; IPR008973; C2_CalB.
InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_RSPS_WWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0068; C2; 1.
Pfam; PF00682; HECT; 1.
Pfam; PF00397; WW; 3.
PRINTS; PR00360; C2DOMAIN.
SMART; SM0019; HECT; 1.
SMART; SM00119; HECT; 1.
                                                                   60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D85414; BAA12803.1; -
                                                                                     Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:97297; Nedd4.
                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Struct. Biol. 8:407-412(2001).
-!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an E2 ubiquitin-conjugating enzyme in the form of a thioester and then directly transfers the ubiquitin to targeted substrates (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 452-499 IN COMPLEX WITH SCNNIB, AND INTERACTION WITH SCNNIA, SCNNIB AND SCNNIG.
MEDLINE=2123577; PubMed=11323714; DOI=10.1038/87562;
Kanelis V., Rotin D., Forman-Kay J.D.;
Solution structure of a Nedd4 ww domain-ENaC peptide complex.";
Nat. Struct. Biol. 8:407-412(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND INTERACTION WITH SCNNIA; SCNNIB AND SCNNIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PATHWAY: Ubiquitin conjugation, third step.
-1- SUBUNIT: Interacts with UBE2D2 (By similarity). Binds SCNNIA, SCNNIB and SCNNIG.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: Ubiquitous. Expression is highest in lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: Contains 1 HECT-type B3 ubiquitin-protein ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney and brain.
-!- MISCELLANEOUS: A cysteine residue is required for ubiquitin-
thiolester formation.
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Staub O., Dho S., Henry P., Correa J., Ishikawa T., McGlade J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na+ channel deleted in Liddle's syndrome."; EMBO J. 15:2371-2380(1996).
                                                                                                                                                                                             Length 887;
                                                                                                                                                                                                                                                 Indels
                                                                                                             854 Ubiquitin (By similarity).
102705 MW; AE7DD3ED63986C50 CRC64;
                                                                                                                                                                                                                                                                                                                                    249 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 286
                                                                                                                                                                                                                                                                                                          38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin-protein ligase Nedd-4 (EC 6.3.2.-).
                                                                                                                                                                                          Score 203; DB 1;
Pred. No. 6.5e-18;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                       1 SPLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    887 AA
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WW 1.
WW 2.
WW 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                          93.1%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U50842; AAB48949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S70642; S70642.
PDB; 115H; NMR; W=450-499
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
  282
438
493
887
854
249
405
460
552
854
887 AA;
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                Ma.
Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Nedd4;
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                                                                                DOMAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NED4 RAT
062940;
                                                                                                                                                                                          Query Match
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blum H., Bauersachs S., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Contains 1 C2 domain.
EMBL; AL137469; CAB70754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                # GOS GO: 0005622; Cintracellular; IEA.

# GOS GO: 0005622; F:ubiquitin-protein ligase activity; IEA.

# GOS GO: 0006512; P:ubiquitin-protein ligase activity; IEA.

# GOS GO: 0006512; P:ubiquitin cycle; IEA.

# InterPro; IPR008973; C2 CalB.

# InterPro; IPR008973; C2 CalB.

# InterPro; IPR001203; WW. Rsp5_WWP.

# Pfam; PP006349; WW.

# Refam; PP00632; WW.

# RANAT; SM00139; HECT; 1.

# SWART; SM00139; HECT; 1.

# SWART; SM00139; HECT; 1.

# SWART; SM00139; HECT; 1.

# RECORD RECOR
                                                                                                                                                                                                                                                                      Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 820;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                      442 AA; 50752 MW; DFF65B3BA6C2D21C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820 AA; 95282 MW; 0FDB34B29B3F4123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp434P2422 (Fragment)
Home sapiens (Human)
                                                                                                                                                                                                                                                                      Score 148; DB 2; I Pred. No. 5.4e-11; 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 177
                                                                                                                                                                                                                                                                                                                                                                                                                   172 PLPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 206
                                                                                                                                                                                                                                                                                                                                                                                 2 PLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.9%; Score 148; DB 2; 71.4%; Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           820 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                        PROSITE; PS50004; C2 DOMAIN 2; 1. PROSITE; PS01159; WW_DOMAIN 1; 1. PROSITE; PS50020; WW_DOMAIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50237; HECT; 1. PROSITE; PS01159; WW DOMAIN 1; 3. PROSITE; PS50020; WW DOMAIN 2; 3. Hypothetical protein.
                                                                                                                                                                                                                                                                      67.9%;
ilarity 71.4%;
Conservative
                         PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 1.
SMART; SM00456; WW; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
Pfam; PF00397; WW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q62940; 115H.
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Testis;
                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
SEQUENCE
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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A MEDLINE=22579291; PubMed=12693553;
A MEDLINE=22579291; PubMed=12693553;
A MEDLINE=22579291; PubMed=12693553;
A Nakajima D., Nagase T., Ohara N., Koga H.;
A Nakajima D., Nagase T., Ohara O., Koga H.;
I "Prediction of the coding sequences of mouse kinah-homologous of the complete nucleotide sequences of 400 mouse KIAA-homologous
T II. The complete nucleotide sequences of cDNA clones
T randomly sampled from size-fractionated libraries.";
T randomly sampled from size-fractionated libraries.";
C -1- SIMILARITY: Contains 1 C2 domain.
R BHBL; AK152283; BAC65565.1; -.
R INTERPO; IPRO00008; C2.
R INTERPO; IPRO00008; C2.
R INTERPO; IPRO00093; C2. Calb.
R InterPro; IPRO01202; WW_Rsp5_WWP.
R Pfam; PF00168; C2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 199; DB 1; Length 887; 86.8%; Pred. No. 2.2e-17; ive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2 domain.
WW 1.
WW 2.
WW 3.
HBCT.
Ubiquitin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102394 MW; D74B1097688CD9A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 SPLPPGWEERQDVLGRTYYVNHESRTTQWKRPSPEDDL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                InterPro; IPR000569; CZ Calb.
InterPro; IPR000569; HECT.
InterPro; IPR000569; HECT.
InterPro; IPR001659; HECT.
InterPro; IPR0016973; CZ; 1.
Pfam; PF00168; CZ; 1.
Pfam; PF00169; CZ; 1.
SMART; SM00239; CZ; 2.
SMART; SM00219; HECT; 1.
SMART; SM0019; HECT; 1.
SMART; SM00499; CZ DOMAIN.
PROSITE; PS0049; CZ DOMAIN 1; 1.
PROSITE; PS0049; CZ DOMAIN 2; 1.
PROSITE; PS0020; HECT; 1.
PROSITE; PS0020; HECT; 1.
PROSITE; PS0020; WW DOMAIN 2; 1.
PROSITE; PS0020; WW DOMAIN 2; 3.
PROSITE; PS0020; WW DOMAIN 2; 3.
PROSITE; PS0020; WW DOMAIN 2; 3.
ID STRUCTURE; Ligase; Repeat; UDI conjugation;
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Name=mKIAA0439;
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Matches 33, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure, Ligase, Re.
Ubl conjugation pathway.
DOMAIN 62 163
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STRAIN=C57BL/6J; TISSUB=Cerebellum;
Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imcerani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsazki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=2079154; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE=Cerebellum;

STRAIN=C57BL/6J; TISSUE=Cerebellum;

STRAIN=C9013; PubMed=11076661; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Amamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatau M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
deriched library, clone:A730011F13 product:neural cell expressed,
Name=Ned41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                        835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB=Cerebellum;
The FANTOM Consortium,
                                                                                      (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN FANTOM Consortium;
                                        PRELIMINARY;
                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                      01-MAR-2003
                                                             Q8BRT9;
                    Q8BRT9
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A MEDINELE FROM N.A.

MEDINELE FROM N.A.

A MOLINELE FROM N.A.

A QI H. Grenier J., Fournier A., Labrie C.;

A QI H. Grenier J., Fournier A., Labrie C.;

A QI H. Grenier J., Fournier A., Labrie C.;

A DI H. Grenier J., Fournier A., Labrie C.;

A DI H. Grenier J., Fournier A., Labrie C.;

T Transcripts in LNCaP human prostate cancer cells.";

MOI. Cell Endocrinol. 210:51-62(2003).

R EMBL; AF210730; AG4524.1;

R EMBL; AF365931; AAM46208.1;

R MSSP; AG5940; 115H.

R HSSP; AG5940; 115H.

R GO; GO:0006622; C:intracellular; IEA.

R GO; GO:00066812; F:ligase activity; IEA.

R GO; GO:00066812; P:ubiquitin-procein ligase activity; IEA.

R GO; GO:00066512; P:ubiquitin-procein ligase activity; IEA.

R GO; GO:00066512; P:ubiquitin-cycle; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21828840; PubMed=11840194; DOI=10.1038/sj.ejhg.5200747; Chen H., Ross C.A., Wang N., Huo Y., MacKinnon D.F., Potash J.B., Simpson S.G., McMahon F.J., DePaulo J.R. Jr., McInnis M.G.; "NEDD4L on human chromosome 18421 has multiple forms of transcripts and is a homologue of the mouse Nedd4-2 gene."; Lanscripts Eur. J. Hum. Genet. 9:922-930(2001).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-UJL-2004 (TrEMBLrel. 27, Last annotation update)
NEDDALA (Ubiquitin ligase NEDD4Lb) (Ubiquitin ligase NEDD4f).
Name-NEDD4La: Synonyms=NEDD4L;
Homo sapiens (Human).
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK042621; BAC31307.1; -.
HSSP; Q62940; 115H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 835;
                                                                                                                       MGD; MGI:1933754; Nedd41.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:000512; F:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW DOMAIN 2; 4.
SEQUENCE 835 AA; 96410 MW; 81C7DD62722DDA9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.9%; Score 148; DB 2; L
71.4%; Pred. No. 1.1e-10;
wiemarches 7;
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Pfam; PP00632; HECT; 1.
Pfam; PF00397; WW; 4.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00403; WWDOMAIN.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002349; WW.
InterPro; IPR001202; WW
                                                                                                                                                                                                                                                                                                  InterPro; IPR002349; WW
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es 25, Conserv
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Pfam, PF00632; HECT; 1.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Astapleron M., Soares M.B., Bonaldon M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rachaguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial malysis of more than 15,000 full-length human
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Skin;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                            67.9%; Score 148; DB 2; Length 854; 71.4%; Pred. No. 1.1e-10; Live 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR008973; CZ GALB.
InterPro; IPR00569; HECT.
InterPro; IPR002349; WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (DEC-2011) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                               Ligase.
SEQUENCE 854 AA; 98180 MW; 00C74E1661F52E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
NEDD4L protein (Hypothetical protein) (Fragment).
Name-NEDD4L;
                                                                                                                                                                                                                                                                                    PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                            2 PLPPGWEERQDILGRIYYVNHESRRIOWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                              855 AA.
                      PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW_DOMAIN_1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002349; WW.
InterPro; IPR001202; WW_Rsp5_WWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EM
EMBL, BC000621, AAH00621.2; --
EMBL, BC019345; AAH19345.1; --
HSSP, Q62940; 115A
                                                                                                                                                            Query Match 67.9%;
Best Local Similarity 71.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
SMART; SM00456; WW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BW58; Q8WUU9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BW58
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0098WS8
001-JJD 0998W
00 N Name 01-JD 0
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S K B B B B
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Kamynina E., Debonneville C., Bens M., Vandewalle A., Staub O.;
"A novel mouse Nedd4 protein suppresses the activity of the epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
                                                                                                                                                                                                                                                                 Length 855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD: WGI1333754; Nedd41.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:000684; F:ligase activity; IEA.

GO; GO:0004842; F:lubiquitin-protein ligase activity; IEA.

GO; GO:0006512; P:ubiquitin gycle; IEA.

GO; GO:0006512; P:ubiquitin gycle; IEA.

InterPro; IPR002349; WW.

InterPro; IPR002349; WW.

PÉam; PF00632; HECT.

PÉam; PF00632; HECT.

PÉam; PF00637; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                              855 AA; 98604 MW; 3CF4A66996F033EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855 AA; 98258 MW; 3BE1566E2C3BA20E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                            Query Match 67.9%; Score 148; DB 2; L
Best Local Similarity 71.4%; Pred. No. 1.1e-10;
Matches 25; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.9%; Score 148; DB 2; L
71.4%; Pred. No. 1.1e-10;
ive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                         PLPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 128
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                                                                                                                                                                                                                                                                                                                                                                        2 PLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 AA.
PRINTS; PR00403; WWDOMAIN.
SWART; SM00119; HECTC; 1.
SWART; SM00456; WW, 4.
PROSITE; PS550237; HECT; 1.
PROSITE; PS501159; WW_DOMAIN_1; 4.
PROSITE; PS501159; WW_DOMAIN_1; 4.
HYDOTHELICAL PROTEIN.
NOW TER
SEQÜENCE 855 AA; 98604 MW; 3CF4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW_DOMAIN_1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ubiquitin-protein ligase Nedd4-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FASEB J. 15:204-214(2001).
EMBL; AF277232; AAK00809.1; -.
HSSP; Q62940; 115H.
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Best Local Similarity 71.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00403; WWDOMAIN.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6 Ncrl BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Na+ channel.";
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73 PLPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 107

RESULT 12

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neural cell expressed, developmentally down-regulated gene 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1993754; Nedd41.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:000442; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0006512; P:ubiquitin cycle; IEA.

InterPro; IPR002349; WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BC039746; AAH39746.1; -.
EMBL: BC071210; AAH71210.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS01020; WW DOMAIN 2; 4.
SEQUENCE PS5020; WW DOMAIN 2; 4.
SEQUENCE 855 AA; 98465 MW; 96C452B442855895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor. C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.9%; Score 148; DB 2; L
71.4%; Pred. No. 1.1e-10;
ive 3; Mismatches 7;
  855 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PP00632; HECT; 1.
Pfam; PP00397; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                      (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00403; WWDOMAIN.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.9%
Best Local Similarity 71.4%
Matches 25, Conservative
 PRELIMINARY;
                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q62940; 115H.
                                                                             Name=Nedd41;
                      01-MAR-2003
QBCFIO
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Klausher R.D., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D., Attschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D., Rad Autschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D., Andren H., Moore T., Max S.I., Wang J., Hsieh F., Dordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Stapelcon M.J., Usdin T.B., Donlyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Ahring M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Bouffard G.G., Shevchenko Y., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Andrews M., Marn M.A., Young D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., The Mail S., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Thuman M. J., Marra M.A., Thuman J. M., Changer R. M., Schein J.E., Jones S.J., Marra M.A., Thuman J. M., Schein J.S., Jones S.J., Marra M.A., Thuman J. M., Schein J.S., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Thuman J.S., Ook S.J., S., Sancha M.J., Thuman J.S., Ook S.J., S., Sancha M.A., Thuman J.S., Ook S.J., S., Sancha M.S., S., Sancha M.S., S., Sancha M.S., S., San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082281; AAH82281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875 AA; 101627 MW; 7662C1958052FC3E CRC64;
                                                                         Created)
Last sequence update)
Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
NEDD4b protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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71.4%; Pred. No. 1.2e-10;
M. M. C. Marches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 PLPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           911 AA
    PRT;
                                                         25-OCT-2004 (TrEMBLrel. 28, C) 25-OCT-2004 (TrEMBLrel. 28, Le 25-OCT-2004 (TrEMBLrel. 28, Le Nedd4l protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.
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PRELIMINARY;
                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
TISSUE=Skin;
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    Q641N8
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Homo sapiens (Human)
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           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buedow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buedow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Minting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:000562; C:intracellular; IEA.
GO; GO:000482; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; F:ubiquitin-protein ligase activity; IEA.
INCEPTO; IPRO0008; C2.
InterPro; IPRO08973; C2. Cal.B.
InterPro; IPRO02569; HECT.
InterPro; IPRO02349; WW.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL; EC032597; AAH32597.1; -.
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PROSITE; PS50004; C2_DOMAIN_2; 1.

PROSITE; PS01159; WW_DOMAIN_1; 3.

PROSITE; PS01159; WW_DOMAIN_2; 3.

SEQUENCE 911 AA; 104921 WW; CE04AAED677AA506 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 1.2e-10;
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71.4%;
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01-OCT-2003 (TrEMBLrel. 25, 10-OCT-2003 (TrEMBLrel. 25, 10-OCT-2004 (TrEMBLrel. 26, 10-OCT-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00403; WWDOMAIN.
SMART; SM00139; CZ; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
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Name=NEDD4L;
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nes 25; Conserv
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1D Q
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DOI=10.1128/MCB.20.22.8526-8535.2000;
Winberg G. Matskova L., Chen F., Plant P., Rotin D., Gish G.,
Ingham R., Ernberg I., Pawson T.;
"Latent membrane protein 2A of Epstein-Barr virus binds Ww domain E3
protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases.";
Mol. Cell. Biol. 20:8526-8535(2000):
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
MEDLINE=22980412; PubMed=14615060; DOI=10.1016/j.mce.2003.08.009;
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             Length 947;
                                                                                                                                                                                            GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016674; F:ligase activity; IEA.
GO; GO:00166742; F:ligase activity; IEA.
GO; GO:0006842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000008; C2.
InterPro; IPR000508; C2.
InterPro; IPR001202; WW_RSP5_WWP.
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71.4%; Pred, No. 1.3e-10;
iive 3; Mismatches 7;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26, NEDD4-like ubiquitin ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SM00239; C2; 1.
SMART; SM0119; HECTc; 1.
SMART; SM00456; WW; 4.
PROSITE; PS00499; C2_DOWAIN
PROSITE; PSS00049; C2_DOWAIN
PROSITE; PSS0037; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 71.4 Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00168; C2; 1. Pfam; PF00632; HECT; 1. Pfam; PF00397; WW; 4.
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RA Okamoto Y., Miyazaki K., Sakamoto M., Kato C., Nakagawara A.;
Subutteed (Sep-2001) to the ENBL/GenBank/DDBJ databases.

CC -1- SIMILARITY: Contains 12 Gonain.

BMB1, ABOJITIS;
BOG 00005052 C: intracellular; IC.

RGO; GO: 000050515; F: protein binding; IPI.

GO; GO: 0000515; F: protein binding; IPI.

GO; GO: 00004827; F: ubiquitin-protein ligase activity; IDA.

RGO; GO: 00004827; F: ubiquitin-protein ligase activity; IDA.

RGO; GO: 00004827; F: ubiquitin-protein ligase activity; NAS.

RGO; GO: 00004827; F: protein ubiquitination; NAS.

RGO; GO: 00004817; P: proditive metal ion; IDA.

RGO; GO: 0004827; P: protein ubiquitination; NAS.

RGO; GO: 00006819; P: proditive metal ion; IDA.

RGO; GO: 00006814; P: sodium ion transport; NAS.

RROO03917; RROO0391; RGCT; I.

RROO03917; RROO0391; RGCT; I.

RROO03917; RROO0391; RGCT; I.

RROO0391; RGCT; RGCT
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Search completed: October 13, 2005, 15:09:16 Job time : 73.381 secs

194 PLPPGWEEKVDNLGRIYYVNHNNRTTQWHRPSLMD 228

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Human NED
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Aae32719 KIAA043 Adeb7542 Prostat Add45762 Human P Adr04136 Human D Adr04135 Human N Adg97132 Human N Abb61355 Drosoph Abb63355 Drosoph Aaw37638 Peptide Adb49230 Novel h Aau87972 Human W Adb49320 Novel h Adb49320 Novel h

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Scoring table:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Run on:

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The present sequence is the WW domain of a HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase. The WW domain binds to the Smad PY motif, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Nedd4.
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ADQ07990
AAW93128
AAW93128
AAE32719
ADE60011
ADD65762
ADR04136
ADR04136
ABG11772
ABB63355
ABB63355
ADB49230
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ADB49326
AAW36797
ADB49320
AAR97683
AAB21979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB83019 standard; peptide; 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-2001 (first entry)
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 Hoekstra MF, Xie W,
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 WO200116604-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB83019;
 Human NED
Human KIA
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Mouse WW
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           2105692 seqs, 386760381 residues
                                                                                                                  October 13, 2005, 14:01:04;
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Listing first 45 summaries
                                                                                  protein search, using sw model
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                                 bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated cell signalling. Agents that ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for treating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
ubiquitin ligase activity. The method is useful for stimulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMF; Smad; cell signalling; inflammation; againg; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Nedd4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 217; DB 4;
100.0%; Pred. No. 1.2e-21;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB83018 standard; peptide; 38 AA
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Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 AA;
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ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; poliomyelitis; HIV; measles; protein therapy; human; NEDD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein complex comprising HECT-RCC1, viral maturation scaffolding protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles,
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                                                                                                                                            96.3%; Score 209; DB 4; 97.4%; Pred. No. 1.4e-20;
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                                                                                                                                                                                                                                                                                                                                       AAE32726 standard; protein; 733
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NEDD4 short form protein.
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31-JUL-2001; 2001US-0308958P.
07-DEC-2001; 2001US-0340170P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-2002; 2002WO-IB002106.
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                              37; Conservative
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N-PSDB; AAD50460.
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                                                                                                                                                                Local Similarity
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                                                                                                            Sequence 38 AA;
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protein (VMSP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides or nucleic acide for identifying a candidate beta-catenin pathway modulating agent or for modulating a beta-catenin pathway of a cell. The invention also relates to a method of modulating a beta-catenin pathway of a pathway in a cell; and diagnosing a disease in a patient by detecting manager to modify the beta-catenin pathway in Drosophila crhologues are able to modify the beta-catenin pathway in Drosophila cells. Beta-catenin (also known as Armadillo in Drosophila) plays a role in cell signalling via the Wingless (Wg) /Wit signalling pathway which is involved in cell cycle progression. Beta-catenin levels are tightly capulated by a complex containing the tumour suppressor proteins APC (adenomateous polyposis coll) and Axin and the serine/threonine kinase GSK3-beta. In the absence of these proteins, beta-catenin accumulates in the induction of target genes such as the cell-cycle regulators cyclin D1 cand c-Myc. The Wingless/beta-catenin signalling pathway is frequently mutated in human cancers, particularly those of the colon. Beta-catenin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying a candidate beta-catenin MBCAT pathway modulating agent, useful for diagnosing and treating cancer, comprises providing an assay system comprising a MBCAT polypeptide or nucleic acid.
                                                                                                                                                                                                                                                                                                                           MBCAT; modifier of beta-catenin; drug screening; beta-catenin pathway; beta-catenin pathway modulator; Wingless signalling pathway; Whit signalling pathway; call cycle progression; diagnosis; cancer; angiogenic disorder; apoptotic disorder; cell proliferation disorder; cytostatic; gene therapy; human; NEDD4; neural precursor cell expressed developmentally downregulated 4.
                                                                                                       Gaps
infection. The invention is also useful in protein therapy. The presegquence is human NEDD4 protein used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the use of MBCAT (modifier of beta-catenin)
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                                                                             Length 733;
                                                                                                    1; Indels
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                                                                                                                                              191 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 228
                                                                                                                               1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                              .
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                                                                                        4e-19;
                                                                              ΩB
                                                                            Score 209; DB
Pred. No. 4e-19
0; Mismatches
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                                                                                                                                                                                                                      ADQ07991 standard; protein; 900 AA
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                                                                          96.3%;
ilarity 97.4%;
Conservative
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-534389/51.
N-PSDB; ADQ07980.
REFSEQ; XM_046129.4.
                                                                                                                                                                                                                                                                                                    Human NEDD4 protein.
                                                                                      Local Similarity
les 37; Conserv
                                                  Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004061123-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                          07-OCT-2004
                           invention
                                                                                                                                                                                                                                                 ADQ07991;
                                                                            Query Match
                                                                                                                                                                                              RESULT 4
                                                                                                                                                                                                           ADQ0799:
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pathway modulating agents identified using the methods of the invention are useful as therapeutic agents for treating disorders associated with defective or impaired beta-catenin function and/or MBCAT function such as cancer, or anglogenic, apoptotic or cell proliferation disorders. Proteins that interact with MBCAT are also useful in detecting and providing information about the function of MBCAT proteins. The present sequence represents a human NED94 (neural precursor cell expressed, developmentally downregulated 4) protein, identified as an MBCAT polypeptide in an example of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ubiquitin-conjugating system; Homologius to E6-Ap carboxyl terminus; ubiquitin, ubiquitination; RSC ligase; KIAAN ligase; UBC4; MAD3; modulator; treatment; proliferative disorder; apoptosis; sepsis; differentiative disorder; apoptosis; sepsis; differentiative disorder; viral infection; tissue wasting disorder; cachexia; malignancy; inflammarcry disease; parasitic disease; tuberculosis; IL-2 therapy; rheumatory disease; parasitic disease; osteoarthritis; gouty arthritis; respiratory distress syndrome; cerebral malaria; chronic pulmonary inflammatory disease; silicosis; pulmonary sarcoidosis; bone resorption disease; reperfusion injury; graft versus host reaction; allograft rejection; Crohn's disease; ulcerative colitis; pyresis; multiple sclerosis; autoimmune diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibitor; ubiquitin-mediated proteolysis; IkappaB polypeptide; HECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying modulators of I-kappa-B proteolysis - used to develop products for treating e.g. proliferative and/or differentiative disorders, infections, tissue wasting, cachexia or AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "partial sequence, no start codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                      96.3%; Score 209; DB 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human KIAAN ligase protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY25170 standard; protein; 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-132274/11.
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 900 AA;
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ubiquitin-mediated proteolysis of a IkappaB polypeptide. The method comprises: (a) providing a ubiquitin-conjugating system including the IkappaB polypeptide and a HECT (Homologous to E6-Ap Carboxyl Terminus) ligase and ubiquitin, to promote ubiquitination of the IkappaB polypeptide by the HECT ligase; (b) contacting the ubiquitin-conjugating system with a candidate agent; (c) measuring a level of ubiquitination of the polypeptide in the presence of the candidate agent and (d) comparing the molypeptide in the presence of the candidate agent is indicative of the IkappaB polypeptide in the absence of the candidate agent; where a statistically significant decrease in ubiquitination of the IkappaB polypeptide in the presence of the candidate agent; where a statistically significant decrease in ubiquitination of the IkappaB polypeptide in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the IkappaB polypeptide in the presence of the modulate binding and/or ubiquitinylation of an IkappaB (or other cellular corral substrate) by a HECT ligase, such as RSC or KIAAN. Such modulate binding and/or ubiquitinylation of an IkappaB (or other cellular or viral substrate) by a HECT ligase, such as RSC or KIAAN. Such modulators can be used e.g. in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, in the treatment of viral infections, and in the treatment of tissue wasting disorders e.g. cachexia secondary to infection or malignancy, cachexia secondary to infection or malignancy, cachexia secondary to infection are malignancy, cachexia secondary to infection are arthritis and other arthritic conditions, secondary arthritis and other arthritic conditions, resorption diseases, incleases, ulcerative colitis, or pyresis, in addition to a number of autoimmune diseases such as multiple sclerosis, autoimmune to a number of autoimmune diseases such as multiple sclerosis, in the invention and in the invention
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Pred. No. 5.3e-19;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 255
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/note= "WW domain"
821. .923
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31-JUL-2001; 2001US-0308958P.
07-DEC-2001; 2001US-0340170P.
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Matches 37; Conservative
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SCCI selected from HETT-WW, HECT-KCL, Gag protein, Gag late domain, Pl3, actin, myosin, HSp60, HSp70, HSp90, STAM1, STAM2A, STAM2B, VHS-UIM,
GTPBSE, E2 enzyme, tSg101, cullin, HBRC1, HERC2, HERC3, Ned44 -like useful for treating viral infections, such as lymphosarcoma, human immunodeficiency virus (HTV), hepatitis, poliomyellitis, measles, or Ebola and for inhibiting budding in a subject. They are also useful in diagnostic assays for determining whether a cell is infected which a virus and for characterising the nature, progression and/or infectivity of the infection. The invention is also useful in protein therapy. The present sequence is human NEDD4 protein used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; Ww binding protein; mouse; ned4; Ww domain.
                                                                                                                                protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles,
                                                                                                             comprising HECT-RCC1, viral maturation scaffolding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.3%; Score 209; DB 6; Best Local Similarity 97.4%; Pred. No. 5.3e-19; Matches 37; Conservative 0; Mismatches 1
                                Alroy I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse WW binding protein Ned4 WW domain #1.
                                Moskowitz H, Reiss Y,
                                                                                                                                                                                              Disclosure; Fig 15; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB49212 standard; peptide; 38 AA
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97US-00826516
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(PROT-) PROTEOLOGICS LTD
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KAY B K.
FOWLKES D M.
                                                               WPI; 2003-111976/10.
N-PSDB; AADS0459.
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                                                                                                                  protein complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 927 AA;
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03-APR-1997;
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                                Greener T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAYB/)
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                                                                                                          invention describes a purified polypeptide (1) comprising a WW domain h has a sequence (S1) selected from 11 sequences fully defined in the ification, a sequence (S2) selected from 48 sequences fully defined
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                                                                                                                            which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 966, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of
                                                                                                                                                                                                                                                                                                                                                                        activities, or as an immunogen to generate antibodies. This is the amino acid sequence of WW binding protein Ned4 WW domain.
                                                                                                                                                                                                                                                                                              the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (1) with the recognition unit. (1) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological
 for discovering polypeptides or as an immunogen to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding Yes proto-oncogene associated protein - used to modulate intracellular signal transduction e.g. for treatment of muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38;
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Pred. No. 2.3e-19;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW domain; signal transduction; diagnosis; gene therapy; Yes proto-oncogene associated protein; YAP; Nedd4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SGLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQDNL
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DELBRUECK CENT MOLECULAR MEDICINE MAX.
discovery, modification and refinement, involved in pharmacological activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR97680 standard; protein; 38 AA.
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                                                                       Example, Fig 5, 133pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.2%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse Nedd4 WW domain-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-286829/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38 AA;
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(DELB-) DELBR
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identified in the Yes proto-oncogene associated proteins (YAPs) of chicken, human and mouse (see also AAR97669-70 and AAR97672). A consensus sequence is given in AAR97671. Mouse Nedd4 plays a role in embryonic development and CNS differentiation. The Nedd4 www domains (AAR97680-82) can be expressed in bacterial, yeast, insect or mammalian cells, and used to identify WW domain ligands. They can be introduced into cells, either directly or by gene therapy, to increase the level of signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW-domain; protein-protein interaction; cell growth regulation; protein degradation regulation; Alzheimer's; Dementia pugilistica; Down's syndrome; Parkinson's disease; Pick's; neurodegenerative; microtubule assembly; tau; hyperplasia; neoplasia; malignancy; psoriasis; retinosis; atherosclerosis; leukaemia; lymphoma; papiloma; pulmonary fibrosis; rhematoid arthritis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mediating protein-protein interactions, useful for regulating cell growth and for treating neurodegenerative disorders, comprises modulating binding of WW domain containing polypeptide with phosphorylated ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for mediating protein-protein interaction, which compristes modulating the binding of a Ww-domain containing peptide with a phosphorylated ligand e.g. tau. WW-domains are highly conserved regions of approximately 40 amino acid residues with two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Down's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invariant tryptophans (W) in a triple stranded beta-sheet. The present sequence is one such WW-domain. When a WW-domain containing peptide is phosphorylated at serine or threonine residues, dephosphorylation of ligands bound to the peptide is inhibited. The present peptide may be useful for mediating protein-protein interaction, regulating cell growth, regulating protein degradation, restoring the function of tau to bind microtubules and promote or restore microtubule assembly in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative diseases e.g. Alzheimer's, Dementia pugilistica, Down'syndrome, Parkinson's disease, Pick's disease, multiple sclerosis, muscular dystrophy, Corticobasal degeneration, Frontotemporal dementias,
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                               Length 38,
                                                                                                                                                                                                             Score 194; DB 2; Length 38 Pred. No. 1.5e-18; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                SGLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                       SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nedd4/mouse peptide containing a WW-domain #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB21978 standard; peptide; 38
                                                                                                                                                                                                               89.4%;
86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-00252404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscular dystrophy; mouse
                                                                                                                                                                                                                                                    33; Conservative
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                     Sequence 38 AA;
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Best Local
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Myotonic dystrophy, Niemann-Pick disease, prion disease with tangles, progressive supranuclear palsy and subacute sclerosing panencephalistis. In addition, inhibitors or stimmlators of interactions between Ww-domains and ligands of the present invention can be used to treat hyperplastic and neoplastic disorders e.g. all forms of malignancies, psoriasis, retinosis, atherosclerosis resulting from plaque formation, leukaemias, benign tumour growth, lymphomas, papilomas, pulmonary fibrosis and rhematoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                 WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein; human; ned4; WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                                                                                                                                                                                Gaps
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                                                                                                                                                       Length 38;
                                                                                                                                                    Score 194; DB 3; Length 38
Pred. No. 1.5e-18;
3; Mismatches 2; Indels
                                                                                                                                                                                                             SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                     SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                                                                                                        Human WW binding protein Ned4 WW domain #1
                                                                                                                                                                                                                                                                                                        ADB49211 standard; peptide; 38 AA
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97US-00826516.
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                                                                                                                                                                     86.88;
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                                                                                                                                                 Query Match
Best Local Similarity 86.8
Matches 33; Conservative
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(KAYB/) KAY B K.
(FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pirozzi G, Kay BK,
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                                                                                                                           Sequence 38 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-APR-1996;
03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW domains (AAR97673-92) were identified in a number of proteins involved in signalling or regulatory functions. The WW domain was initially identified in the Yes proto-oncogene associated proteins (YAPs) of chicken, human and mouse (see also AAR97669-70 and AAR97672). A consensus sequence is given in AAR97671. Mouse Need4 plays a role in embryonic development and CNS differentiation. The Nedd4 WW domains (AAR97680-82).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be expressed in bacterial, yeast, insect or mammalian cells, and used to identify WW domain ligands. They can be introduced into cells, either directly or by gene therapy, to increase the level of signal transduction
activities, or as an immunogen to generate antibodies. This is the amino acid sequence of WW binding protein Ned4\ WW\ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Yes proto-oncogene associated protein - used to modulate intracellular signal transduction e.g. for treatment of muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                        Length 38;
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                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                            WW domain; signal transduction; diagnosis; gene therapy;
Yes proto-oncogene associated protein; YAP; Nedd4.
                                                                                                                                  1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                   SPLPPGWEERQDVLGRIYYVNHESRRIQWKRPSPDDDL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLPPGWEEKQDDRGRSYYVDHNSKTTTWSKPTMQDD 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 146; DB 2;
64.9%; Pred. No. 4.3e-12;
iive 6; Mismatches 7
                                                                        Score 194; DB 7;
Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELBRUECK CENT MOLECULAR MEDICINE MAX.
                                                                                                    3; Mismatches
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                                                                                                                                                                                                                                         38
                                                                          89.4%;
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                                                                                                                                                                                                                                        AAR97681 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen H, Bork P;
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 64.9
Matches 24; Conservative
                                                                                                       33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                  Mouse Nedd4 WW domain-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-286829/29.
                                                                        Query Match
Best Local Similarity
Matches 33; Conserv
                                            Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9617061-A1.
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RESULT 12

The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 49 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (1) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the drug candidate, and determining the effect, if any, of the presence of the amount of the candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological

ADB49214

Mus sp.

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The invention describes a purified polypeptide (I) comprising a Ww domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S3) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the amount of the drug candidate, and determining the effect, if any of the presence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate antibodies. This is the amino acid sequence of WW binding protein Ned4 WW domain.
                                                               candidate screening, drug discovery, drug modification, immunogen, WW binding protein, human, ned4, WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                      Human WW binding protein Ned4 WW domain #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fowlkes DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example, Fig 5, 133pp; English.
                                                                                                                                                                                                                                                                                  28-JUN-2002; 2002US-00185050.
                                                                                                                                                                                                                                                                                                                              96US-00630916.
97US-00826516.
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Best Local Similarity 68.6
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-635075/60
                                                                                                                                                                                                                                                                                                                                                                                                (PIRO/) PIROZZI G.
(KAYB/) KAY B K.
                                                                                          drug refinement;
                                                                  WW domain; drug
                                                                                                                                                                                     US2003077577-A1
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                                                                                                                                                                                                                                                                                                                              03-APR-1996;
03-APR-1997;
                                                                                                                                                                                                                                   24-APR-2003
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AAW13386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGLPPGWEEKQDDRGRSYYVDHNSKTTTWSKPTMQDD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 146; DB 7;
Pred. No. 4.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                               Mouse WW binding protein Ned4 WW domain #2.
                          ADB49214 standard; peptide; 38 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fowlkes DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example, Fig 5, 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2002; 2002US-00185050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00630916.
97US-00826516.
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAY B K.
FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pirozzi G, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-635075/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PIRO/) PIROZZI G.
(KAYB/) KAY B K.
(FOWL/) FOWLKES D N
                                                                                                                                                                                                                                                                                                                                US2003077577-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1996;
03-APR-1997;
                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                            24-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies.
                                                                      ADB49214;
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Gaps
                                                                                                                                                                                                                     Protein ubiquitin ligase; pub2; cdc25 phosphatase; CDK kinase; p53; cell cycle; transgenic animal.
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0
65.0%; Score 141; DB 7; Length 38; 68.6%; Pred. No. 2e-11;
                       Indels
                       7;
                                               35
                                                             1 SGLPPGWEERQDILGRIYYVNHESRRTQWKRPTPQ
           Pred. No. 2e-1
4; Mismatches
                                                                                                                                                                                              Human protein ubiquitin ligase pub3.
                                                                                                                              AAW13386 standard; protein; 818
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ADB49215 standard; peptide; 38

RESULT 13

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ADB49215

Matches

04-DEC-2003 (first entry)

ADB49215;

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154 LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 187
                                                                                                                                                                                                                                                                                                               Search completed: October 13, 2005, 15:00:32 Job time : 86.6044 secs
                                                                                                                                                                          Sequence 830 AA;
                                                                                                                                                                                                   Query Match
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Matches
g
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                                                                                                                                                                                                                                                                                      Human protein ubiquitin ligases publ (AAW13384), pub2 (AAW13385) and pub3 (AAW13386) are homologues of fission yeast publ (AAW13387) and were identified from cDNA clones (AAT47040-42) obtd. e.g. from a keratinocyte CDNA library. Pub polypeptides can be proded in transfected host cells. They can control the steady state level of cdc25 phosphatase, the degree of CDK kinase (e.g. cdc2) dephosphorylation and the steady state level of p53 (controlling the degree of cell cycle regulation of p53). They can regulate cell or tissue differentiation, or cell growth or proliferation by affecting other proteins, can be a specific (ant)agonist of wild type protein function and may be used as immunogens to elicit a specific
                                                                                                                                                                                                               Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 141; DB 2; Length 818; 70.6%; Pred. No. 6.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated sequence HP4-08-005, SEQ ID 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LPPGWEERQDILGRIYYVNHESRRTQWKRPTPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                 Claim 1; Page 87-91; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                   Nefsky B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ97134 standard; protein; 830
                                                                                                                          COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY INC.
                                                                                                 95US-00539205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2002; 2002US-00330773
                                                                         96WO-US015930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morris DW, Malandro MS;
                                                                                                                                                   Caligiuri M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-543781/52
                                                                                                                                                                          WPI; 1997-226206/20
N-PSDB; AAT47042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 818 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004060304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    immune residue
                                                                                                                                                                                                                                       proliferation.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                       WO9712962-A1
                                                                         04-OCT-1996;
                                                                                                  04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                10-APR-1997
                                                                                                                                                   Beach D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ97134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                           (COLD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating
                                                                                                                                                                                                                        The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphona. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 65.0%; Score 141; DB 8; L Local Similarity 70.6%; Pred. No. 6.6e-10; les 24; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LPPGWEERQDILGRIYYVNHESRRIQWKRPIPQD 36
                                                                                                                                                     Claim 1; SEQ ID NO 110; 199pp; English.
                                           contiguous nucleotides, useful for dia:
cancers such as leukemia and lymphoma.
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 13, 2005, 13:50:53 ; Search time 18.0952 Seconds

(without alignments)

156.763 Million cell updates/sec
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(Without Alighments)
Title: US-09-385-918-4
Perfect score: 217
Sequence: 1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata1/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata1/1/iaa/6A\_COMB.pep:\*

3: /cgn2\_6/ptodata1/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata1/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata1/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata1/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Query				
No.	Score	Match	Length	BB	QI	Description
1	209	96.3	927	т	US-08-895-601-6	Sequence 6, Appli
7	200	92.2	38	ო	US-08-630-916A-18	18,
m	194	89.4	38	~	US-09-066-074-11	11,
4	194	89.4	38	7	US-08-555-912A-11	11,
'n	194	89.4	38	٣	US-08-630-916A-17	17,
9	194	89.4	38	ო	US-08-348-518C-13	13,
7	194	89.4	38	ო	US-08-476-509B-13	13,
æ	194	89.4	38	4	US-09-252-404A-36	36,
σ	194	89.4	38	4	US-09-275-900-11	11,
10	146	67.3	38	ო	US-08-630-916A-20	20,
11	146	67.3	38	ო	US-08-348-518C-14	Sequence 14, Appl
12	146	67.3	38	m	US-08-476-509B-14	14,
13	141	65.0	38	6	US-08-630-916A-21	21,
14	141	65.0	834	m	US-08-539-205A-6	9
15	141	65.0	834	4	US-09-392-163A-6	Sequence 6, Appli
16	135	62.2	38	٣	US-08-630-916A-36	36,
17	132	60.8	38	~	-990-60-	Sequence 12, Appl
18	132	60.8	38	7	US-08-555-912A-12	12,
19	132		38	ო	-08-630-916A-1	19,
20	132	60.8	m	ᠬ	-08	16,
21	132	60.8	m	ო	US-08-476-509B-16	16,
22	132	60.8	6	4	US-09-252-404A-37	37,
23	132	60.8	38	4	US-09-275-900-12	12,
24	126		89	4	US-09-248-796A-18186	181
25	123	56.7	166	m	US-08-539-205A-4	4
56	123	56.7	166	4	US-09-392-163A-4	4, 4
27	122	56.2	683	ო	US-08-630-916A-46	46,

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906 3 US-08-630-916A-48 30 4 US-09-252-404A-3 38 3 US-08-630-916A-35 39 US-09-774-639-371 4 US-09-919-039-235 852 2 US-09-910-039-235 852 2 US-09-970-060-3 854 2 US-09-977-746-4 38 3 US-09-630-916A-31 38 3 US-08-630-916A-31 38 3 US-08-630-916A-31 38 3 US-08-630-916A-31 38 3 US-08-630-916A-32 38 3 US-08-630-916A-31 38 3 US-08-630-916A-21 38 3 US-08-630-916A-21 38 3 US-08-630-916A-21 38 3 US-08-630-916A-21	4 W W W W W W W W W W W W W W W W W W W	Sequence 2, Appli Sequence 24, Appl Sequence 15, Appl Sequence 15, Appl
~ C W 4 K K K K K K K K K K K K K K K K K K	US-08-630-916A-48 US-09-252-404A-3 US-08-630-916A-35 US-09-774-639-371 US-09-919-039-235 US-09-357-746-3 US-09-357-746-4 US-08-357-746-4 US-08-630-916A-32 US-08-630-916A-31 US-08-630-916A-32 US-08-630-916A-31 US-08-630-916A-31 US-08-630-916A-31	US-09-392-163A-2 US-08-630-916A-24 US-08-348-518C-15 US-08-476-509B-15
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US-08-995-601-6
Sequence 6, Application US/0895601
Sequence 6, Application Strack, Peter J.
APPLICANT: Beta-Koneto, Peggy
APPLICANT: Glass, Susan J.
TITLE OF INVENTION: RECLIED AND REAGENTS RELATED THERETO
ONDRESSES: 16
ONDRESSES: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COMPUTER: ISH PC Compatible
OPERATING SYSTEM: PC-ONDS-1005
SOFTWARE: ISH PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION UNGER: US/08/85-005
SOFTWARE: ISH PC-ULL-1997
CLASSIPICATION UNGER: US/09/85-601
FILING DATE: 132-1000
STATCHERY APPLICATION WHERE WP.
FILING DATE: 132-1000
STATCHERY APPLICATION UNGER: US/09/85-601
FILING DATE: 133-1000
STELEDWART: USA
CONDUTER: SATISTATION UNGER: MATCHEW P.
REGISTRATION UNGER: WATCHEW P.
REGISTRATION UNGER: MATCHEW P.
REFERENCE/ONCHINGER: MATCHEW P.
REPRESCOMMUTION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICAT
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13.NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.8
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: Nedd4/Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-555-912A-11
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             Sequence 18, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
APPLICANT: PITOZZI, Gregorio
APPLICANT: RAY, Brian K.
APPLICANT: POLIVERION:
TITLE OF INVERTION: DESTRICTED HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CONTRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CONTRY: New York
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: NEW YORK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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Patent No. 5922467

GENERAL INFORMATION:

APPLICANT HUNCE et al., Tony
ITILE OF INVENTION:

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown; MOLECULE TYPE: peptide
US-08-630-916A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 38 amino
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
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ZIP: 92037
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US-08-630-916A-18
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Gaps
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ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN DATA:
APPLICATION NUMBER: US/08/555,912A
FILING DATE: 13-NOV-1995
GIASSIFICATION: 435
ATTORNEY AGIENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/011001
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5070
TELEPAX: 619/678-5070
TELEPAX: 619/678-5070
TELEPAX: 619/678-5099
INPORMATION POR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TENNEY AGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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Patent No. 5972697

GENERAL INFORMATION:

APPLICANT: Hunter et al., Tony

TITLE OF INVENTION: NIMA INTERACTING PROTEINS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STRET: 4225 Executive Square, Suite 1400

CITY: La Jolla
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 194; DB 2;
Pred. No. 1.5e-20;
3; Mismatches 2,
                                                                                                                                                                                                          RAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/011001
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 aming acids
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A SH2 DOMAIN ASSOCIATED PROTEIN, A SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE SIGNALLING DOMAIN THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
TITLE OF INVENTION: A SH2 DOWAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Klubber & Jackson
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                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: 0.1-DEC-1994
ATTOREY/AGENT INFORMATION:
NAME: Jackson ESQ, David A
ATTOREY/AGENT INFORMATION:
NAME: Jackson ESQ, David A
REGISTRATION NUMBER: 26,742
REPERBNCE/DOCKET NUMBER: 26,742
REPERAX: 201 343-1684
TELEPAX: 201 343-1684
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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Pred. No. 1.5e-20;
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Patent No. 6034212
GENERAL INFORMATION:
TITLE OF INVENTION: A SH2 DOMAIN TITLE OF INVENTION: SIGNALLING DO TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 26 CORRESPONDENCE ADDRESS: ADDRESSE: Klauber & Jackson
                                                                                                                                                                                                                STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.4%;
ilarity 86.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o: protein
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserval
                                                                                                                                                                                                                                                                                New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mouse-1
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                          07601
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                                                                                                                                                                                                                                                                                                                COUNTRY:
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Sequence 17, Application US/08610916A

Betath No. 6011137

GENERAL INFORMATION:
APPLICANT: Birozi, Gregorio
APPLICANT: Ray, Brian K.
APPLICANT: Rowikes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: IDENTIFICATION AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

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                                                                                                                      89.4%; Score 194; DB 2; Length 38;
86.8%; Pred. No. 1.5e-20;
iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OFTWARE: PATENTING SYSTEM: PC-UOS/MS-LUOS
SOFTWARE: PATENTIN PC-UOS/MS-LUOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION ISOPO-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acide
                                                                                                                                                                                                                                                                                   1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
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Patent No. 6022740
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.0
                                                                                                                                                                                   33; Conservative
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; IMMEDIATE SOURCE:
; CLONE: Nedd4/Mouse
US-08-555-912A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-630-916A-17
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CITY: La Jolla
                                                                                                                                                                    COUNTRY: USA
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Patent No. 6495376
GENERAL INFORMATION:
APPLICANT: Kun Ping Lu
APPLICANT: Kao Zhen Zhou
TITLE OF INVENTION: Methods and Compositions for Regulating
TITLE OF INVENTION: Protein-Protein Interactions
FILE REFERENCE: 1440.1034-000
CURRENT APPLICATION NUMBER: US/09/252,404A
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%; Score 194; DB 3; Length 38; 86.8%; Pred. No. 1.5e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

89.4%; Score 194; DB 4;
Best Local Similarity 86.8%; Pred. No. 1.5e-20;
Matches 33; Conservative 3; Mismatches 2.
                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
TELEFAX: 201 343-1684
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
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Sequence 11, Application US/09275900
Patent No. 6596848
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mouse-1
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-476-509B-13
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LENGTH: 38
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Sequence 20, Application US/08630916A

Patent No. 6011137

GENERAL INFORMATION:
Patent No. 6011137

GENERAL INFORMATION:
Prozzi, Gregorio
APPLICANT: Pizozzi, Gregorio
APPLICANT: Prozzi, Gregorio
APPLICANT: Powlkes, Dana M.
TITLE OF INVENTION: DENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STREET: New York
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                                                                                                                                                                                                                                     ZIP: 92037

COMPUTER READABLE FORM:
    MEDLUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATE: US/09/275,900
    FILING DATE: 24-Mar-1999
    CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 38;
APPLICANT: Hunter et al., Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 38
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COUNTRY: United States
ZIP: 10036-271
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIN: FO-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.4%; Score 194; DB 4;
86.8%; Pred. No. 1.5e-20;
tive 3; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07251/011001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/555,912
FILING DATE: 13.NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nedd4/Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.8
Matches 33; Conservative
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Sequence 14, Application US/08476509B
Sequence 15, Application US/08476509B
Sequence 10, Application US/08476509B
Sequence 10, Marius
APPLICANT: SUDOL, MARIUS
APPLICANT: HENRY, CHEN
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: 6 Jackson
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                  ö
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                                                                                                                                                     67.3%; Score 146; DB 3; Length 38;
64.9%; Pred. No. 9.7e-14;
tive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.3%; Score 146; DB 3; Length 38 Best Local Similarity 64.9%; Pred. No. 9.7e-14; Matches 24; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCETAILING STILLING Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B FILING DATE: U1-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: JGC&SON ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 187-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                   1 SGLPPGWEEKQDDRGRSYYVDHNSKTTTWSKPTMQDD 37
                                                                                                                                                                                                                                          1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDN 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                Query Match
Best Local Similarity 64.9°
Matches 24; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
    internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mouse-2
IMMEDIATE SOURCE:
CLONE: Nedd4
                        ORIGINAL SOURCE:
ORGANISM: Mouse-2
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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  FRAGMENT TYPE:
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                                                                                                          US-08-348-518C-14
                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-476-509B-14
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US-08-348-518C-14
Sequence 14, Application US/08348518C
SENERAL INFORMATION:
APPLICANT: BEER, DORK
APPLICANT: BEER, DORK
APPLICANT: HERRY, CHEN
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
MUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Aver---
CITY: Hackensack Aver---
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146; DB 3; Length 38
Pred. No. 9.7e-14;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER EAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: 01-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET NUMBER: 26,742
REFERENCE/POCKET NUMBER: 600-1-101
TELECOMMUNICATION INFORMATION:
TELEFPHONE: 201 343-1684
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
                                                                                                                                                         1101-203
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-2
TELECHONE: (212) 790-9090
TELEPAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 aming acids
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 64.9
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                                             FILING DATE: 03
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               US-08-630-916A-20
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Sequence 6, Application US/09392163A
Patent No. 6503742
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefesty, Bradley
TITLE OF INVENTION: Upiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.0%; Score 141; DB 3; Length 834; 70.6%; Pred. No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 832-1000
TELEFAX: (617) 832-7000
                                                                                                                                                                               NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
                                                                                                                                                                                                                                                                                         TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              : 834 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 70.6
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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US-09-392-163A-6
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APPLICANT: Beach, David H.
APPLICANT: Bach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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65.0%; Score 141; DB 3; Length 38;
Best Local Similarity 68.6%; Pred. No. 5e-13;
Matches 24; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
CUNTRY: United States
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LUMBUTH: 38 aming acids
         1 SGLPPGWEEKQDDRGRSYYVDHNSKTTTWSKPTMQDD 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQ 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-539-205A-6
Sequence 6, Application US/08539205A
; Patent No. 6001619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
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Query Match 65.0%; Score 141; DB 4; Length 834; Best Local Similarity 70.6%; Pred. No. 1.9e-11; Matches 24; Conservative 3; Mismatches 7; Indels 0; Gaps

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8 qq Search completed: October 13, 2005, 14:03:05 Job time : 19.2202 secs

THE PACE PLANT WOOD

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us-09-385-918-4.rapb

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1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-10-307-956-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 38; Conserv
                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, 2
Sequence 16,
Sequence 15,
Sequence 18,
Sequence 17,
Sequence 17,
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-307-956-4

US-10-307-956-3

US-10-097-534-16

US-10-097-534-15

US-10-185-050-18

US-10-185-050-17

US-10-687-36-11

US-10-687-36-11

US-10-616-379-11

US-10-616-379-11
                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                            1859788 seqs, 416717961 residues
                                           October 13, 2005, 13:59:34;
                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                              protein search, using sw model
                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                         seq length: 0
seq length: 200000000
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217
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Match 1
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Perfect score:
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2209
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244
21194
444
1444
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Maximum DB
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                                            Run on:
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279, App
31439, A
3, Appli
9, Appli
275, App
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16857, A
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19, Appl
7, Appli
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3162, Ap
4, Appli
8162, Ap
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12, Appl
12, Appl
12, Appl
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ALIGNMENTS
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Seed to the control of the control o Gaps .. 0 14; Length 38; 100.0%; Score 217; DB 14; llarity 100.0%; Pred. No. 1.8e-21; Conservative 0; Mismatches 0;

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Sequence 3, Application US/10307956
; Publication NorUS20030119072A1
; Sequence 3, Application US/10307956
; Publication NorUS20030119072A1
; GAPERAL INFORMATION:
    APPLICANT: Xie, Weilin
; APPLICANT: Marcurio, Frank
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; TITLE OF INVENTION: MUMBER: US/10/3056
; CURRENT APPLICATION NUMBER: US/10/3056
; CURRENT APPLICATION NUMBER: US/09/385,918
; PRIOR APPLICATION NUMBER: US/09/385,918
; RIOR PILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10097534

Sequence 10. Application US/10097534

Publication No. US20030049607A1

GENERAL INFORMATION:

APPLICANT: GREENER, TSVIKA

APPLICANT: RISS, YUVAL

APPLICANT: RISS, YUVAL

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL

TITLE OF INVENTION: MATURATION

FILE REFERENCE: PLV-001.01

CURRENT APPLICATION NUMBER: 60/275,224

PRIOR FILING DATE: 2001-07-31

SOFTWARE: PATENTIN NUMBER: 60/340,170

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.3%; Score 209; DB 14; Length 38; Best Local Similarity 97.4%; Pred. No. 2.1e-20; Matches 37; Conservative 0; Mismatches 1; Indels
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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Best Local Similarity
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; Sequence 15, Application US/10097534 ; Publication No. US20030049607A1

RESULT 4 US-10-097-534-15

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RESULT >
VS-10-18
VS-10-18, Application US/10185050
Sequence 18, Application US/10185050
Publication No. US2003007757A1
GENERAL INFORMATION: Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: DENTIFICATION AND DOMAINS AND METHODS OF USING SAME
            APPLICANT: REISS, YUVAL
APPLICANT: REISS, YUVAL
APPLICANT: REISS, YUVAL
APPLICANT: REISS, YUVAL
TAPLICANT: REISS, YUVAL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
FILE REPERENCE: PLV-001.01
CURRENT APPLICATION NUMBER: 05/205,224
PRIOR APPLICATION NUMBER: 60/275,224
PRIOR APPLICATION NUMBER: 60/301-03-12
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR PILING DATE: 2001-07-31
PRIOR PRILING DATE: 2001-07-31
PRIOR PELING DATE: 2001-07-31
PRIOR PELING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 15
LENGTH: 927
TYPE: PRI
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MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 209; DB 14
Pred. No. 6e-19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 18
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Best Local Similarity 97.4%;
Matches 37; Conservative
TSVIKA
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8 Db

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Gaps
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86.8%; Pred. No. 2.1e-18;
tive 3; Mismatches 2; Indels
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86.8%; Pred. No. 2.1e-18;
tive 3; Mismatches 2;
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10687361
Fublication No. US20040101896A1
GENERAL INFORMATION:
APPLICANT: Hunter, Tony
ITILE OF INVENTION: NIMA INTERACTING PROTEINS
FILE REFERENCE: 66671-078
CURRENT APPLICATION NUMBER: US/10/687,361
CURRENT APPLICATION NUMBER: US/10/687,361
CURRENT APPLICATION NUMBER: US 10/616,410
PRIOR FILING DATE: 2003-10-15
PRIOR FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20050027107A1
GENERAL INFORMATION:
APPLICANT: Hunter, Tony
APPLICANT: Hanes, Stewen D.
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
FILE REPERENCE: 66671-085
CURRENT APPLICATION NUMBER: US/10/716,379
                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
      28-Jun-2002
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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Best Local Similarity 86.8%
Matches 33; Conservative
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Best Local Similarity 86.8°
Matches 33; Conservative
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ORGANISM: Mus musculus
US-10-687-361-11
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APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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Sequence 36, Application US/10256865

Publication No. US20330049672A1

GENERAL INFORMATION:

APPLICANT: Kun Ping Lu

APPLICANT: Kiao Zhen Zhou

TITLE OF INVENTION: Methods and Compositions for Regulating

TITLE OF INVENTION: Protein-Protein Interactions

FILE REFERENCE: 1440.1034-000

CURRENT APPLICATION NUMBER: US/10/256,865

CURRENT FILING DATE: 2002-09-26

PRIOR FILING DATE: 1999-02-18
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                                                                                                                                                                           92.2%; Score 200; DB 14; Length 38; 94.7%; Pred. No. 3.4e-19; tive 0; Mismatches 2; Indels
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Pred. No. 2.1e-18;
3; Mismatches 2; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
                                                                                                                                                                                                                                                                                                 1 SPLPPGWEERQDILGRIYYVNHESRRIQWKRPIRQDNL 38
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ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown
MOLECTLE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.48;
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Best Local Similarity 86.8°
                                                                                                                                                                                                                         36; Conservative
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: mouse
US-10-256-865-36
                                                                                                                                    US-10-185-050-18
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Thu Oct 13 15:32:47 2005

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Conservative
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US-10-185-050-20
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Pred. No. 2.1e-18;
3; Mismatches 2;
                                                                                                                                                                                               Score 194; DB 17;
Pred. No. 2.1e-18;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 194; DB 17;
Pred. No. 2.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/10648631
Fublication No. US20050049404A1
GENERAL INFORMATION:
APPLICANT: Hunter, Tony
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
FILE REFERENCE: 66671-044
CURRENT APPLICATION NUMBER: US/10/648,631
CURRENT FILING DATE: 2003-08-25
PRIOR FILING DATE: 2003-08-05
NUMBER OF SEQ 1D NOS: 22
SOFTWARE: FASTERO FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hunter, Tony
APPLICANT: Hunter, Tony
APPLICANT: Kun Ping, Lu
TITLE OF INVENTION: NIMA INTERACTING PROTEINS
FILE REFERENCE: 66671-043
CURRENT APPLICATION NUMBER: US/10/616,410
CURRENT FILING DATE: 2003-07-08
PRIOR PELICATION NUMBER: US 09/275,900
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ 1D NOS: 22
SOFTWARE: FASTSEQ for Windows Version 4.0
CURRENT FILING DATE: 2003-11-17
PRIOR APPLICATION NUMBER: US 10/616,410
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                          US-10-616-410-11
; Sequence 11, Application US/10616410
; Publication No. US20050033032A1
; GENERAL INFORMATION:
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86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.8
Matches 33; Conservative
                                                                                                                                                                                                                                     33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                           TYPE: PRT
CRGANISM: Mus musculus
US-10-716-379-11
                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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LENGTH: 38
                                                                                        SEQ ID NO 11
LENGTH: 38
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LENGTH: 38
                                                                                                                                                                                                                                   Matches
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Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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Gaps
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Publication No. US200300775771
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 38;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                 1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURENT APPLICATION DATA:
APPLICATION WHRER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIPICATION -UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 119,872
REGISTRATION NUMBER: 119,97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBEHONE: (212) 790-999
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDN 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
67.3%; Score 146; DB 14;
Best Local Similarity 64.9%; Pred. No. 5.5e-12;
Matches 24; Conservative 6; Mismatches 7;
                                                                                1 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-185-050-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENN1E
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        Sequence 20, Application US/10185050 Publication No. US20030077577A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    APPLICANT: Pirozzi, Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
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3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
COUNTRY: USA
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APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHOGS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Best Local Similarity 70.6%; Pred. No. 6.5e-10;
Matches 24; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 141; DB 14; 70.6%; Pred. No. 6.7e-10; tive 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 107
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/392,163
FILING DATE: <UNKNOWN-
APPLICATION NUMBER: US 08/539,205
FILING DATE: <UNKNOWN-
ATTORNEY/ABENT INFORMATION:
NAME: VINCENT, MALTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECHONNICATION INFORMATION:
TELECHONE: (617) 832-1000
TELEFAX: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
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CURRENT APPLICATION NUMBER: US/10/205,823

CURRENT FILING DATE: 2002-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR FILING DATE: 2001-08-25

SOUTHARRE: FRANCE OF WINDOWS VERSION 4.0

SEQ ID NOS: 455

SEQ ID NOS: 455
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-313-955-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 277, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARĀCTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gannavarapu, Manjula
Gorbatcheva, Bella
Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
Zhao, Xumei
                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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US-10-205-823-277
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-205-823-277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICANT:
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     POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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APPLICANT: Beach, David H.
Caliguri, Maureen
Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DATE: PLOSS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/185,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-Jun-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 119,972
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.0%; Score 141; DB 14;
68.6%; Pred. No. 2.5e-11;
iive 4; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SGLPPGWEEKQDERGRSYYVDHNSRTTTWTKPTVQ 35
                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/313,955
FILING DATE: 05-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-185-050-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10313955 Publication No. US20030199036A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                           SEQUENCES: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.6'
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-313-955-6
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95 25

Search completed: October 13, 2005, 14:50:00 Job time: 81.011 secs

Thu

protein search, using sw model OM protein October 13, 2005, 14:36:01; Search time 15.8681 Seconds (without alignments) 230.414 Million cell updates/sec Run on:

US-09-385-918-4

1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

probable ubiquitin ubiquitin-protein ubiquitin-protein hypothetical prote Pini protein - hum peptidylproly1 iso 45K WW domain-cont 45K WW domain-cont ubiquitin ligase N ubiquitin-protein ubiquitin-protein ubiquitin protein yes-associated pro brain-specific ang yes-associated pro formin binding pro hypothetical prote nuclear protein EM yes-associated pro hypothetical WW do probable ubiquitin prote probable guanylate Pinl protein homol prote synaptic scaffoldi protein C43E11.3 hypothetical Description \$66562 T37545 T47801 \$68520 JC7136 JC7507 S70642 T46412 S43217 T39585 T49744 T14152 T33637 JE0209 Query Match Length 1616 163 163 383 386 1277 691 472 1171 1256 448 78.5 76.5 75.5 74.5 74.7 72 72 Result

	hypothetical prote	hypothetical prote	protein F13E6.4 (i	integrase-like pro	hypothetical prote	hypothetical prote	ESS1 protein - yea	hypothetical prote	hypothetical prote	protein 2K1098.1 [	hypothetical prote	probable transcrip	formin binding pro	acrosomal major pr	probable cell wall
T20274	S30014	T26779	G89632	S22571	T19825	T23160	S52764	869038	S40923	F88557	T40617	T08599	S64716	JX0347	T40618
7	~ (	7	7	~	~	N	~	7	7	0	~	0	7	7	7
889	583	120	457	499	837	1012	170	465	695	724	143	1098	26	180	273
32.7	32.3	30.9	30.9	30.9	30.9	30.4	29.3	29.0	29.0	29.0	28.8	28.3	28.1	27.9	27.9
71	70	67	67	67	67	99	63.5	63	63	63	62.5	61.5	61	60.5	60.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

## ALIGNMENTS

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down-regulated expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui F;40-77/Domain: WW repeat homology «WW1>
F;196-233/Domain: WW repeat homology «WW2>
F;151-228/Domain: WW repeat homology «WW3>
F;317-682/Domain: WW repeat homology «WW3>
F;317-682/Domain: ubiquitin-protein ligase homology «UBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                               C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000 C.Accession: 183196 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000 C.Accession: 183196 #sequence_revision 02-Aug-1996 #siochem. Biophys. Res. Commun: 185, 1155-1161, 1992 A;Title: Identification of a set of genes with developmentally down-regulate A;Reference number: 160167; MUID:92328780; PMID:1378265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                           A;Accession: 183196
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-708 <RES>
A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
A;Gene: NEDD-4
NEDD-4 ORF - mouse (fragment)
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.8
Matches 33; Conservative
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## 1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38 40 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 77 g ð

ubiquitin ligase Nedd4 - rat (fragment)
(Species: Rattus norvegicus (Norway rat)
(Cjate: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004
(CjAccession: 870642
(RjStaub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
(RjStaub, O.; Bho, S.; Henry, P.C.; Correa, D.; Ishikawa, T.; McGlade, J.; Rotin, D.
(RjStaub, O.; Bho, S.; Henry, P.C.; Forman J.; Ishikawa, T.; McGlade, J.; Rotin, D.
(RjStaub, O.; McGlade, Jane, P.; McGlade, J.; Rotin, D.)
(RjStaub, O.; McGlade, Bind to the proline-rich PY motifs in the epithelial Na(+))
(RjStaub, O.; McGlade, MuID:96221297; PMID:8665844) A,Accession: S70642 A,Status: preliminary, nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 1-887 <STA>

A, Cross-references: UNIPROT: Q62940; EMBL: U50842; NID: g1293646; PIDN: AAB48949.1; PID: g129 C, Genetics:

C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui F;54-167/Domain: protein kinase C C2 region homology <KC2> F;246-283/Domain: WW repeat homology <WW1> A;Gene: Nedd4

hypothetical prote

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protein; binds and ubiqu

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Gaps

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Indels

Length 809;

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A,Accession: T39585
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-786 <VOL>
A,Cross-references: UNIPROT:014326; EMBL:299759; PIDN:CAB16903.1; GSPDB:GN00067; SPDB:SP
A,Experimental source: strain 972h-; cosmid c16E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable ubiquitin-protein ligase [imported] - Neurospora crassa
Nalternate names: protein B24B19.160
C;Alternate names: protein B24B19.160
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T4974
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
                                                                                    A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein and FUR4 pr
WW repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology F;236-273/Domain: WW repeat homology <WWR1>F;306-343/Domain: WW repeat homology <WWR2>F;364-401/Domain: WW repeat homology <WWR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.9%; Score 130; DB 2; Length 786; 62.9%; Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T39585 – – – – – – – – – – – StyOlckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, August 1997 A;Reference number: Z21865
        ;Reference number: S70050; MUID:96154942; PMID:8596462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.8%; Score 132; DB 1; L/71.0%; Pred. No. 6.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 LPPGWERRADSLGRTYYVDHNTRTTTWTRPASSTN 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDN 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 LPPGWERRIDNFGRIYYVDHNTRITTWKRPI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LPPGWEERQDILGRTYYVNHESRRTQWKRPT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: involved in endocytosis of GAP1 C; Superfamily: yeast ubiquitin-protein ligase;
                                                                                                                                                                                                                                                          A,Gene: SGD:RSP5; PUB1; NP11; MIPS:YER125w
A,Cross-references: MIPS:YER125w; SGD:S000927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;229-266/Domain: WW repeat homology <WW1>
F;331-368/Domain: WW repeat homology <WW2>
F;387-424/Domain: WW repeat homology <WW3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 22, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SPDB:SPBC16E9.11c
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                         A; Residues: 1-101 <HEI>
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-815 <SCH>
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                                                                                                                                                                                                                                                                                                                                                   A; Map position: 5R
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                                                                                                                                                                                                                           C;Genetics:
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A;Note: DKFZp434P2422.1
C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T46412

ubiquitin protein ligase (EC 6.3.2.19) NEDD4 - human (fragment)

ubiquitin protein ligase (EC 6.3.2.19) NEDD4 - human (fragment)

Ujalernate names: hypothetical protein DKFZp434P2422.1

CjSpecies: Homo sapiens (man)

CjSpecies: Homo sapiens (man)

CjBete: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

CjBete: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

CjBete: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

KjBlum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Ajacesion: T46412

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                                                                                                                                                                              Length 887;
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70.6%; Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                              2; Indels
F;402-439/Domain: WW repeat homology <WW2>
F;459-496/Domain: WW repeat homology <WW3>
F;555-881/Domain: ubiquitin-protein ligase homology <UBI>
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$132-139/Domain: WW repeat homology <WWR2>
F;390-430/Domain: WW repeat homology <WWR3>
F;489-814/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                                                                     246 SPLPPGWEERQDVLGRTYYVNHESRTTQWKRPSPEDDL 283
                                                                                                                                                                                                                                                                                                                                                        1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL 38
                                                                                                                                                                         87.6%; Score 190; DB 2;
84.2%; Pred. No. 2.8e-16;
ive 4; Mismatches 2;
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                                                                                                                                                        Ouery Match
Best Local Similarity 84.2'
Matches 32; Conservative
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Best Local Similarity
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Gaps

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A;Cross-references: UNIPROT:092462; EMBL:Z99161; PIDN:CAB16207.1; GSPDB:GN00066; SPDB:SF A;Cross-references: UNIPROT:092462; EMBL:Z99161; PIDN:CAB16207.1; GSPDB:GN00066; SPDB:SF R;Saleki, R.; Jia, Z.; Karagiannis, J.; Young, P.G. Mol. Gen. Genet. 254, 520-528, 1997
Mol. Gen. Genet. 254, 520-528, 1997
A;Title: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ ub A;Reference number: 207985; MUID:97340937; PMID:9197411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description: involved in of the mitotic activating tyrosine phosphatase cdc25 (validat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 3
A;Introns: 7/1; 205/3; 250/1; 656/3; 713/3; 794/3; 964/3; 1232/3; 1298/3; 1445/3; 1523/3
A;Note: F24G16.40
F;508-545/Domain: WW repeat homology <WWR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Description: involved in of the mitotic activating tyrosine phosphatase (Function: 4TOL)
A; Description: equired for low pH-tolerance (validated, MUID:97340937)
C; Supering tyrosat ubiquitin-protein ligase; WW repeat homology
C; Keywords: cell cycle control; ligase
F; 205-242/Domain: WW repeat homology < www.>
F; 288-325/Domain: WW repeat homology < www.>
F; 382/Domain: WW repeat homology < www.>
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A;Cross-references: UNIPROT:Q9M1Z7; EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 2; Len. 9.1e-08;
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48.5%; Pred. No. 1.9e-05;
live 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Map position: 1
A.Introns: 6/2; 14/1; 62/2
C.Function: <UB1>
A.Description: EC 6.3.2.19 [validated, MUID:96205868]
C.Function: <CYC>
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A;Molecule type: DNA
A;Residues: 1-767 <SAL>
                preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 LPPGWERRTDNLGRTYYVDHNTRSTTWIRP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 9.16
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LPPGWEERQDILGRTYYVNHESRRTQWKRP 32
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Pred. No. 9
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70.0%;
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Best Local Similarity 70.09
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: publ; SPDB: SPAC11G7.02
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Best Local Similarity 48.5'
Matches 16; Conservative
                                             A; Molecule type: DNA
A; Residues: 1-767 <MCL>
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Pin1 protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Useful Section of the protein ligase (EC 6.3.2.19) - fission yeast (Schizosaccharomyces pombe)

NyAlernate names: B6-AP-like protein ubiquitin ligase
C,Species: Schizosaccharomyces pombe
C,Species: Schizosaccharomyces pombe
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C,Accession: S65652; T4159
R,Necfeky, B.; Baach, D.
EMBO J. 15, 130-1312, 1996
A,Title: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25
A,Residues: S65622; MUID:96205868; PMID:8635463
A,Residues: 10-1312, 1996
A,Title: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of A,Residues: 1-766 «NEF-A,Cross-references: UNIPROT:092462; GB:U66716; NID:g1519443; PIDN:AAB07514.1; PID:g15194
A,Residues: 1-766 «NEF-A,Cross-references: UNIPROT:092462; GB:U66716; NID:g1519443; PIDN:AAB07514.1; PID:g15194
A,Residues: 1-766 and E. Library, August 1996
A,Residues: 1-766 and E2-AP-like protein ubiquitin ligase in the degradation of A,Reference number: Z22935
A,Accession: T45159
A,Accession: T45159
A,Residues: 1-766 and A,Reference number: Z22935
A,Residues: 1-766 and A,
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ubiquitin-protein ligase (EC 6.3.2.19) publ [validated] - fission yeast (Sch NyAlternate names: ubiquitin ligase Publ
NyAlternate names: ubiquitin ligase Publ
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37545; T48655
R;McLean, J; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V. A;Reference number: Z21722
A;Reference number: Z21722
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A;Cross-references: EMBL:ALJ56192; GSPDB:GN00116; NCSP:B24B19.160
A;Experimental source: BAC clone B24B19; strain OR74A
C;Genetics:
A;Gene: Cs.
A;Gene: Cs.
A;Map position: 6
A;Introns: 11/1; 24/1; 59/2; 110/1; 783/2
C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology c;S39-276/Domain: WW repeat homology cWWR1>
F;339-276/Domain: WW repeat homology cWWR3>
F;393-430/Domain: WW repeat homology cWWR3>
                                                                                                                                                                                                                                                                                                                                                     Length 815
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70.0%; Pred. No. 9.1e-08;
ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                               59.9%; Score 130; DB 2; 71.0%; Pred. No. 1.2e-08; ive 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LPAGWERREDHLGRIYYVDHNSRTISWNRPT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LPPGWEERQDILGRTYYVNHESRRTQWKRPT 33
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Best Local Similarity 70.01
Best Local 21; Conservative
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Matches 22; Conservative
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protein

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C; Comment: This protein participates in a variety of cellular processes, such as
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Best Local Similarity 38.9%
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A; Residues: 1-1277 <HIR>
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JC7508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T14152
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                                                       C;Genetics:
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C;Species: Homo sapiens (man)
C;Date: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession.
S68520
A;Title: A human peptidyl-prolyl isomerase essential for regulation of mitosis.
A;Accession: S68520
A;Title: A human peptidyl-prolyl isomerase essential for regulation of mitosis.
A;Accession: S68520
A;Status: preliminary; nucleic acid sequence not shown
A;Accession: S68520
A;Status: preliminary; nucleic acid sequence not shown
A;Nolecule type: mRNA
A;Residues: 1-163 < LUK>
A;Cross-references: UNIPROT:Q13526; EMBL:U49070; NID:g1332709; PIDN:AAC50492.1; PID:g133
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Cross-references: GDB:5218381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptidylprolyl isomerase (EC 5.2.1.8) - mouse
Deptidylprolyl isomerase (EC 5.2.1.8) - mouse
N;Alternate names: parvulins, Pin1 protein
C;Species: Mus musculus (house mouse)
C;Accession: JC7136
G;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:090UR7; DDBJ:AB009691; NID:g6468199; PIDN:BAA87037.1; PID:g6
C;Comment: This protein is a member of peptidyl prolyl cis/trans isomerase family. It is
tes in oligopeptides, controls G2/M transition of HeLa cells, regulates entry into G1 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45K WW domain-containing protein - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7507

R;Valverde, P.

R;Valverde, P.

R;Valverde, P.

A;Aitle: Cloning, expression, and mapping of hWW45, a novel human WW domain-containing A;Reference number: JC7507; MUID:20483619; PMID:11027580

A;Accession: JC7507

A;Molecule type: mRNA

A;Residues: 1-383 <VAL>
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C,Superfamily: yeast ESS1 protein; WW repeat homology
(Keywords: cis-trans-isomerase; mitosis
F,5-43/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.9%; Score 97.5; DB 2; 53.1%; Pred. No. 3.3e-05;
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Pred. No. 3.2e-05;
5; Mismatches 9;
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Best Local Similarity 53.1%;
Matches 17; Conservative
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JC7507
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Biochem. Biophys. Res. Commun. 276, 990-998, 2000
A;Title: Cloning, expression, and mapping of hWW45, a novel human WW domain-containing gc
A;Reference number: JC7507; MUID:20483619; PMID:11027580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synappic scaffolding protein S-SCAM - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Mar-2004
C;Accession: T14152
R;Hirao, K.; Hata, Y.; Ide, N.; Takeuchi, M.; Irie, M.; Yao, I.; Deguchi, M.; Toyoda, A.
B;Hirao, K.; Hata, Y.; Ide, N.; Takeuchi, M.; Irie, M.; Yao, I.; Deguchi, M.; Toyoda, A.
A;Title: A novel multiple PDZ domain-containing molecule interacting with N-methyl-d-asps
A;Reference number: 217889; MUID:98361985; PMID:9694864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of cellular processes, such as protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: may assemble receptors and cell adhesion proteins at synaptic junctions F;3102-339/Domain: WW repeat homology <WW1>F;348-385/Domain: WW repeat homology <WW2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45K WW domain-containing protein - mouse
C;Species: Mus musculus (house mouse)
C;Dete: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7508
R;Valverde, P.
A;Gene: ww45
A;Map position: 14q13-21, 14q21-23
C;Keywords: coiled coil; myristylation; protein degradation; transcription
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                                                                                                                           Length 383;
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41.9%; Score 91; DB 2; Le
Best Local Similarity 38.9%; Pred. No. 0.00055;
Matches 14; Conservative 6; Mismatches 16;
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Pred. No. 0.0064;
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38.9%; Pred. No. 0.00055;
tive 6; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8VEB2; GB:AJ292968 C;Comment: This protein participates in a variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 LPYGWEKIDDPIYGTYYVDHINRRTQFENP 379
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Search completed: October 13, 2005, 15:11:15 Job time : 16.8681 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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October 13, 2005, 14:03:23; Search time 72.381 Seconds (without alignments) 268.842 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-385-918-4 217 1 SGLPPGWEERQDILGRIYYVNHESRRIQWKRPTPQDNL 38 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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QI	NED4_HUMAN	Q9N134	NED4 MOUSE	NED4_RAT	080003	Q9NT88	Q8BRT9	Q9H2W4	Q9BW58	Q99PK2	QBCFI0	Q641N8	Q8N5A7	Q7Z5F1	Q96PUS	Q7Z5F2	Q7Z5N3	043165	Q7QE76	Q8QGJ2	Q7KUR2	Q95R64	Q95TQ0	QBIQR6	Q9VVI3	Q6DIR6	042573	Q6GMDS	Q7PQR5	RSP5_YEAST	Q75AI2
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132	132	131	130	130	130	123	122	122	121.5	121.5	121	121	121
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# ALIGNMENTS

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O90134;
O1-0CT-2000 (TEMBLrel. 15, Created)
O1-0CT-2000 (TEMBLrel. 25, Last sequence update)
O1-0CT-2001 (TEMBLrel. 25, Last annotation update)
Ubiquitin-protein ligase Nedd4 (Fragment).
Ubiquitin-protein ligase Nedd4 (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Greger R.;
"The distal convoluted tubule of rabbit kidney does not express functional sodium channel.";
Am. J. Physiol. Renal Physiol. 280:F530-F539(2001).
EMBL; AF229024; AAF45194.1; -.
HSSP; Q62940; 115H.
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MEDLINE=21113801; PubMed=11181416;
Velazquez H., Silva T., Andujar E., Desir G.V., Ellison D.H.,
                                                                                                                                                                                                                                                                                                          Score 209; DB 1; Length 1000;
Pred. No. 8.1e-19;
0; Mismatches 1; Indels (
                                                                                                                                    PROSITE; PS0049; C2 DOMAIN 1; 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50237; HEGT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS502030; WW DOMAIN 1; 4.
Ligase; Repeat; Ubl Conjugation; Ubl conjugation pathway.
DOMAIN 9 44
                                                                                                                                                                                                                                                                                         3728088E50C149CB CRC64;
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C2 domain.
Poly-Gln.
WW 1.
WW 2.
WW 3.
WW 4.
HECT.
Ubiquitin (By similarity).
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InterPro; IPR0018973; C2 Calb.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PF00397; WW. 4.
     Genew; WGNC:7727; NEDD4.
H-InvDB; HIX0012269; -.
MIM, 602278; -.
InterPro; IPR000008; C2.
InterPro; IPR000973; C2 CaLB.
InterPro; IPR0000569; HECT.
InterPro; IPR001202; WW_Rsp5_WWP.
Pfam; PP00168; C2, 1.
Pfam; PP00168; C2, 1.
Pfam; PP001697; WW; 4.
PRINTS; PP00360; C2DOMAIN.
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PROSITE; PS01159; WW_DOMAIN_1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
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                                                                                                                                                                                                                                                                                                            96.3%;
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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nes 37; Conservative
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SEQUENCE FROM N.A.

SEQUENCE TISSUE-Thymus;

SEQUENCE TISSUE-Thymus;

MEDININE_25354683; PubMed=12466851; DOI=10.1038/nature01266;

ANDELINE_25354683; PubMed=12466851; DOI=10.1038/nature01266;

ANDELINE_25354683; PubMed=12466851; DOI=10.1038/nature01266;

ANDELINE_25354683; PubMed=12466851; DOI=10.1038/nature01266;

ANDELINE_25354683; PubMed=12466851; DOI=10.1038/namaka I., Kiyosawa H., Aradaci I., Kiyosawa H., Aradaci I., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Fletcher C.F., Forrest A., Frazer K.S., Baldare J.A., Bradt D., Burusic V., Chothia C., Corbai L.E., Cousins S., Baldare J.A., Bradta D., Harvisc V., Chothia C., Corbai L.E., Cousins S., Arani A., Kawaji H., Kawasawa Y., Kaczierski R.M., King B.L., Arani A., Kawaji H., Kawasawa Y., Kaczierski R.M., King B.L., Kanajott D.R., Matlatis L., Marchionni L., McKenzle L., Miki H., A. Magashima T., Nummata K., Pohitus J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada Y., Walls S., Mallang L.G., Wangler C., Wang Y., Walanabe Y., Walls E., Wallming L.G., Wynshaw-Boris A., Yanagisawa M., Sakazume N., Sato K., Haran. Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Sato K., Haran. A., Hashizume W., Imcoani K., Ishii Y., Itoh M., Kagawa I., Haran. Hashizume W., Imcoani K., Ishii Y., Shinagawa A., Haran. Hashizume W., Satoki D., Shibata K., Shinagawa A., Haran. Hashizume W., Sasaaki D., Shibata K., Shinagawa A., Haran. Hashizume W., Sasaaki D., Shibata K., Shinagawa A.,
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"Identification of a set of genes with developmentally down-regulated
expression in the mouse brain." 185:1155-1161(1992).
Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                       Length 455;
                                                                                                                                                                                                                                         Indels
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
      51811 MW; D1C4549B52E22298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDSL 135
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                                                               Score 204; DB 2,
"red, No. 1.6e-18;
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MEDLINE=92328780; PubMed=1378265;
                                                                                                                       94.0%;
94.7%;
                                                                                                                                                                                                                                  Conservative
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455 AA;
                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                              Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakajima D., Nagase T., Ohara O., Koga H.;
"Prediction of the coding sequences of mouse homologues of KIAA gene:
"Prediction of the coding sequences of 400 mouse KIAA-homologous
conplete nucleotide sequences of 400 mouse KIAA-homologous
conplete nucleotide sequences of consoling sequences of consolin
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation 60, 770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: Brain.
-i- MISCELANEOUS: A cysteine residue is required for ubiquitin-
thiolester formation.
-i- SIMILARITY: Contains 1 C2 domain.
-i- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Involved in the embryonic development and differentiation of the central nervous system.

PATHWAY: Ubiquitin conjugation; third step.
SUBUNIT: Binds SCNNIA, SCNNIB and SCNNIG (By similarity). STRECELLULAR LOCATION: CYCOPlasmic.
TISSUE SPECIFICITY: Brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 3 WW domains. CAUTION: Ref.3 sequence differs from that shown due to a frameshift in position 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:97297; Nedd4.

GG; GG:0005829; C:cytosol; IDA.

GG; GG:0000151; C:ubiquitin ligase complex; IPI.

GG; GG:000551; F:protein binding; IPI.

GG; GG:0004842; F:ubiquitin-protein ligase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ligase, Repeat, Ubl Conjugation, Ubl conjugation pathway. DOMAIN 65 166 C2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U96635; AAB63360.1; ALT_FRAME.
                                                                                                                                          TISSUE=Brain;
MEDLINE=22579291; PubMed=12693553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00499; C2 DOMAIN 1; 1. PROSITE, PS50004; C2 DOMAIN 2; 1. PROSITE; PS50237; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01159; WW DOMAIN 1; 3. PS50020; WW DOMAIN 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000008; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_Rsp5_WWP.
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EMBL, AK089767; BAC40558.1; --
EMBL, AK122203; BAC65485.1; --
HSSP; Q62940; 115H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D85414; BAA12803.1; -
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
PRINTS; PR00360; C2DOMAIN.
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       similarity)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRUCTURE BY NMR OF 452-499 IN COMPLEX WITH SCNNIB, AND INTERACTION
WITH SCNNIA, SCNNIB AND SCNNIG
WITH SCNNIA, SCNNIB AND SCNNIG
MEDLINE-21223577; PubMed=11323714; DOI=10.1038/87562;
Kanelis V., Rotin D., Forman-Kay J.D.;
Kanelis V., Rotin D., Forman-Kay J.D.;
Nat. Struct. Biol. 8:407-412 (2001)
-!- FUNCTION: E3 ubiquitin-protein ligase which accepts ubiquitin from an Ez ubiquitin-conjugating enzyme in the form of a thioseter and then directly transfers the ubiquitin to targeted substrates (By
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND INTERACTION WITH SCNNIA; SCNNIB AND SCNNIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Ubiquitous. Expression is highest in lung.
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-!- SUBUNIT: Interacts with UBE2D2 (By similarity). Binds SCNNIA,
SCNNIB and SCNNIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kidney and brain.
-!- MISCELLANBOUS: A cysteine residue is required for ubiquitin-thiolester formation.
-!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na+ channel deleted in Liddle's syndrome."; EMBO J. 15:2371-2380(1996).
                                                                                                                                                                                              Score 194; DB 1; Length 887;
Pred. No. 7e-17;
3; Mismatches 2; Indels
                                                                                                             854 Ubiquitin (By similarity).
102705 MW; AE7DD3ED63986C50 CRC64;
                                                                                                                                                                                                                                                                                                                                         249 SPLPPGWEERQDVLGRTYYVNHESRRTQWKRPSPDDDL 286
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25-OCT-2004 (Rel. 45, Last annotation update)
E3 ubiquitin-protein ligase Nedd-4 (EC 6.3.2.-).
                                                                                                                                                                                                                                                                                                               1 SGLPPGWEERQDILGRTYYVNHESRRTQWKRPTPQDNL
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WW 1.
WW 2.
HECT.
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PDB; 115H; NMR; W=450-499
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Q62940;
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Pfam; PF00397; WW; 1
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X MEDLINE=22579291; PubMed=12693553;

A Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

A Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

Nakajima D., Nagase T., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

T makajima D., Nagase T., Ohara R., Inamoto S., Aizawa H., Yuasa S.,

T in The complete nucleotide sequences of 400 mouse KIAA-homologous compact mucleotide sequences of 400 mouse KIAA-homologous T randomly sampled from size-fractionated libraries.",

DNA Res. 10:35-48(2003)

C -!- SIMILARITY: Contains 1 C2 domain.

R HSSP; Q13526; 1PIN.

R InterPro; IPR000008; C2.

R InterPro; IPR001202; WW_RSP5_WWP.

R Pfam; PF00168; C2; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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84.2%; Pred. No. 2.4e-16;
ive 4; Mismatches 2; Indels
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Last annotation update)
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                                 InterPro; IPR008973; C2_Calb.
InterPro; IPR008973; C2_Calb.
InterPro; IPR008973; C2_Calb.
InterPro; IPR000569; HECT.
InterPro; IPR00168; C2; 1.
Pfam; PP00168; C2; 1.
Pfam; PP00397; WW; 3.
PRINTS; PR00360; C2DOMAIN.
SWART; SW0019; HECTc; 1.
SWART; SW0019; HECTc; 1.
SWART; SW00456; WW; 3.
PROSITE; PS50004; C2_DOMAIN 1; 1.
PROSITE; PS50004; C2_DOMAIN 1; 1.
PROSITE; PS500159; WW DOMAIN 1; 3.
PROSITE; PS50020; WW_DOMAIN 1; 3.
PROSITE; PS50020; WW_DOMAIN 1; 3.
DROSITE; PS50020; WW_DOMAIN 1; 3.
DROSITE; PS50020; WW_DOMAIN 1; 3.
DROSITE; PS50020; WW_DOMAIN 2; 3.
3D-structure; Ligase; Repeat; Ubl conjugation; Domain
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Name=mKIAA0439;
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Best Local Similarity 84.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Testis;
Blum H., Badersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL, AL137469; CAB70754.1;
-- HSSP, Q62940; 115H.
                                                                                                                                                                                                                                                                                          .;
0
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GO; GO:0005622; C:intracellular; IEA.

GO; GO:0006442; P:ubiquitin-protein ligase activity; IEA.

GO; GO:0006542; P:ubiquitin cycle; IEA.

InterPro; IPR000008; C2.

InterPro; IPR000569; HECT.

InterPro; IPR002349; WW.

InterPro; IPR002349; WW.

InterPro; IPR001202; WW.Rep5_WWP.
                                                                                                                                                                                     442 AA; 50752 MW; DFF65B3BA6C2D21C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp434P2422 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.0%; Score 141; DB 2; ilarity 70.6%; Pred. No. 7.1e-10; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                     Score 141; DB 2;
Pred. No. 3.6e-10;
                                                                                                                                                                                                                                                                                                                                                                    173 LPPGWEEKVDNLGRTYYVVHNNRSTQWHRPSLMD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 177
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                                                                                                                                                                                                                                                                                       3; Mismatches
PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS50159; WW DOMAIN 1; 1.
PROSITE; PS5020; WW DOMAIN 1; 1.
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Pfam; PF00168; C2; 1.
Pfam; PF00182; HECT; 1.
Pfam; PR004039; WW; 3.
PRINTS; PR004039; WWDOWAIN.
SNART; SM00239; C2; 1.
SNART; SM00119; HECT; 1.
PR0ART; SM00416; WW; 3.
PR0SITE; PS50004; C2 DOMAIN.
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PROSITE; PS01159; WW DOMAIN 1; 3.
PROSITE; PS50020; WW DOMAIN 2; 3.
Hypothetical protein.
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.6%;
Matches 24; Conservative
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InterPro;
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Q9H2W4;
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     SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Cerebellum;

MEDLINE=C57BL/6J; TISSUE=Cerebellum;

MEDLINE=C57BL/6J; TISSUE=Cerebellum;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Itoh M., Akiawa T., Ritsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumcto H., Sakaguchi S., Ikegami T., Kashiwada A.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRANT=C57BL/G1 TISSUB=Cerebellum;
MEDLINE=C57BL/G49374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=C9798.74; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium, the Right Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Haranco K., Hiraokar T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagwa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakazume N., Sano H., Sasaic C., Sakazume N., Sano H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRIN=CS7BL/6G; TISSUE-Cerebellum;
MEDLINE=99279213; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                              01-MAR 2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730011F13 product:neural cell expressed,
developmentally down-regulated gene 4b, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUm;
                                                   835 AA
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
                                                   PRT;
                                                                                            (TrEMBLrel. 23,
                                                PRELIMINARY;
                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                            Name=Nedd41;
                                              Q8BRT9
RESULT 7

1008RT9

RESULT 7

RESULT 7

RESULT 101-M

DT 01-M

RESULT 7

RESULT 8

RESULT 8
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINES-29804012.

Qi H., Grenier J., Fournier A., Labrie C.;

"Androgens differentially regulate the expression of NEDD4L

ranscripts in LNGaP human prostate cancer cells.";

MOI. Cell. Endocrinol. 210:51-62(2003).

EMBL, AF210730; AAG43524.1;

EMBL, AF310533; AAM46208.1;

EMBL; AY112983; AAM76728.1;

HSSP; Q62940:115H.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-UUJ-2004 (TrEMBLrel. 27, Last annotation update)
NEDD4La (Upiquitin ligase NEDD4Lb) (Ubiquitin ligase NEDD4f)
Name=NEDD4La; Synonyms=NEDD4L;
Homo sapiens (Human)
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AK04251; BAC31307.1; ... HSP, O62940; IISH. MGD; MGI:1933754; Nedd41. GO; GO:0005622; C:intracellular; IEA. GO; GO:0005622; C:intracellular; IEA. GO; GO:0005612; P:ubiquitin-protein ligase activity; IEA. GO; GO:0005512; P:ubiquitin cycle; IEA. IEA. IIDERPO; IPR000569; HECT.
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GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
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70.6%; Pred. No. 7.3e-10;
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PROSITE; PS01159; WW DOMAIN 1; 4.

PROSITE: PS50020; WW DOMAIN 2; 4.

SEQUENCE 835 AA; 96410 MW; 810
                                                                                                                                                                                                                                                                               InterPro; IPR002349; WW.
InterPro; IPR001202; WW.Rsp5_WWP.
Pfam; PF00632; HECT; 1.
Pfam; PP00397; WW; 4.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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SMART; SM00119; HECTC; 1.
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nes 24; Conserv
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PRELIMINARY;
Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
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SEQUENCE
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                                                                                                                                                                                                                                                                             Query Match
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MEDINES-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINES-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Atlaschaf R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wubin G.M., Heibh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rhey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Miscaley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                              Length 854;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC000621; AAH00621.2;
EMBL; BC019343; AAH19345.1;
HSSP; Q62940; 115H.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:iubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR008973; C2 CalB.
InterPro; IPR002349; WW.
                                                                                                                                                         Score 141; DB 2; Length 85
Pred. No. 7.5e-10;
3; Mismatches 7; Indels
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                              854 AA; 98180 MW; 00C74E1661F52E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UUN-2001 (TrEMBLrel. 17, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
NEDD41, protein (Hypothetical protein) (Fragment).
Name-NED041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                  PRT;
                   PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
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                                                                                                                                                            65.0%;
                                                                                                                                    Query Match
Best Local Similarity 70.0.
Best Local 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
  SMART; SM00456; WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BW58; Q8WUU9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue=uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Skin;
                                                                                           Ligase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BW58
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1098W18
10098W18
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MBDILNB=21067027; PubMed=11149908;
Kamynina E., Debonneville C., Bens M., Vandewalle A., Staub O.;
"A novel mouse Nedd4 protein suppresses the activity of the epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                    855 AA; 98604 MW; 3CF4A66996F033EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         855 AA; 98258 MW; 3BE1566E2C3BA20E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 65.0%; Score 141; DB 2; I
Best Local Similarity 70.6%; Pred. No. 7.5e-10;
Matches 24; Conservative 3; Mismatches 7;
                                                                                                                                                                                        65.0%; Score 141; DB 2; I
70.6%; Pred. No. 7.5e-10;
Live 3; Mismatches 7;
                                                                                                                                                                                                                                                                                            95 LPPGWEEKVDNLGRTYYVNHNNRTTQWHRPSLMD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 107
                                                                                                                                                                                                                                                                  3 LPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LPPGWEERQDILGRIYYVNHESRRTQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                          855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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PROSITE; PS01159; WW_DOMAIN_1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                      PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN_1; 4.
PROSITE; PS50020; WW DOMAIN_2; 4.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ubiquitin-protein ligase Nedd4-2.
Name=Nedd41;
PRINTS; PR00403; WWDOMAIN.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
                                                                                                                                                                                                        Local Similarity 70.6
nes 24; Conservative
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LPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 107

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor. C3;

MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

XI ausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Judin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

M. Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                              01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neural cell expressed, developmentally down-regulated gene 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 855;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS01159; WW DOWAIN 1; 4.
PROSITE; PS50020; WW DOWAIN 2; 4.
SEQUENCE 855 AA; 98465 WW; 96C452B442855895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.0%; Score 141; DB 2; L
Best Local Similarity 70.6%; Pred. No. 7.5e-10;
Matches 24; Conservative 3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
                                Created)
                           (TrEMBLrel. 23, (TrEMBLrel. 23, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sednences.
PRELIMINARY;
                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA
                                                                                                              Name=Nedd41;
                               01-MAR-2003
01-MAR-2003
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A Straubberg R.L., Feingold E.A., Grouse J.G.,

Ra Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ra Altschul S.P., Zeeberg B. Buerow K.H., Schaefer C.F., Bhar N.K.,

Ra Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Ra Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleron M., Usdin T.B., Torchivuki S., Carninci P., Prange C.,

Rapas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rapas S.S., McEwan P.J., McKernan K.J., Malke J.A., Gunarane P.H.,

Rapas S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rapas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rapas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rapas S., Worley W.C., Nackernan M., Madan A., Rodrigues S., Sanchez A.,

Rapakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rapakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rapakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rapas S.J., Marra M.J.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rapas S.J., Marra M.J.,

Rapas
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                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             875 AA; 101627 MW; 7662C1958052FC3E CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
NEDD4L protein.
                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%; Score 141; DB 2; 70.6%; Pred. No. 7.7e-10; tive 3; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 LPPGWEEKVDNLGRTYYVNHNNRSTQWHRPSLMD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LPPGWEERQDILGRIYYVNHESRRIQWKRPTPQD 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12477932; DOI=10.1073/pnas.242603899;
PRT;
                                                                   25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC082281; AAH82281.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.",
                                                                                                                                                                                                 Nedd41 protein (Fragment).
Name=Nedd41;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8N5A7;
                                              0641NB
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Q641NB
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3 LPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36 

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947 AA;
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Matches 24; Conserv
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                          SEQUENCE FROM N.A.
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NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=NEDL3;
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        Riabsher R.D., Feinged E.A., Grouse L.H., Depres. 120, 2011.

Riabsher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rapleron M., Soares M.B., Bonaldon M.F., Carannor P.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carannor P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McEwan P.J., McKernan K.J., Make J.A., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeshey D., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Ganes S.J., Marra M.A.,
Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Name-NEDD4L;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 911;
                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:000562; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin-protein ligase activity; IEA.
InterPro; IPR00008; C2.
InterPro; IPR00569; HECT.
InterPro; IPR002569; HECT.
InterPro; IPR001209; WW. RSp5_WWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                     Strauberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 C2 domain.
EMBL, BC012597; AAH32597.1; -.
HSSP; Q62940; 115H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW_DOMAIN_1; 3.
PROSITE; PS01159; WW_DOMAIN_2; 3.
SEQUENCE 911 AA; 104921 WW; CE04AAED677AA506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 LPPGWEEKVDNLGRTYYVNHNNRTTOWHRPSLMD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.0%; Score 141; DB 2; 70.6%; Pred. No. 8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00403; WWDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00239; C2; 1.
SMART; SM00119; HECTC; 1.
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nes 24; Conservative
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00456; WW; 3.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE=20501262; PubMed=11046148;
DOI=10.1128/MCB.20.22 8526-85355.2000;
Winberg G., Matskova L., Chen F., Plant P., Rotin D., Gish G.,
Ingham R., Ernberg I., Pawson T.;
"Latent membrane protein 2A of Epstein-Barr virus binds Ww domain E3
protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases.";
Mol. Cell. Biol. 20:8526-8535(2000):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
MEDLINE=22980412; PubMed=14615060; DOI=10.1016/j.mce.2003.08.009; Qi H., Grenier J., Fournier A., Labrie C.; "Androgens differentially regulate the expression of NEDD4L transcripts in LNCaP human prostate cancer cells."; Mol. Cell Endocrinol. 210:51-62(2003).

-! SIMILARITY: Contains 1 C2 domain.

BMBL; AY112985; AAM76730.1; -.

HSSP; Q62940; 115H.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 947;
                                                                                                                                                                                                                                            GO; GO:0005622; C:intracellular; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
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70.6%; Pred. No. 8.4e-10;
Michael 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LPPGWEERQDILGRTYYVNHESRRTQWKRPTPQD 36
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                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000008; C2.
InterPro; IPR008973; C2_CalB.
InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_Rsp5_WWP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel. 26, NEDD4-like ubiquitin ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00239; C2; 1.
SMART; SM00119; HECTc; 1.
SMART; SM00456; WN; 4.
PROSITE; PS000499; C2_DOWAIN
PROSITE; PS500049; C2_DOWAIN
PROSITE; PS50037; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00168; C2; 1.
Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Length 955;
                                                                                          955 AA; 110021 MW; A8BB278A37F6A6B5 CRC64;
                                                                                              Query Match 65.0%; Score 141; DB 2; Lo
Best Local Similarity 70.6%; Pred. No. 8.5e-10;
Matches 24; Conservative 3; Mismatches 7;
                                                                                        Ligase.
SEQUENCE
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195 LPPGWEEKVDNLGRTYYVNHNNRTTOWHRPSLMD 228 3 LPPGWEERQDILGRIYYVNHESRRIQWKRPTPQD 36 δ 요

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Gaps

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Indels

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October 13, 2005, 14:01:04; Search time 85.6044 Seconds (without alignments) 171.684 Million cell updates/sec Run on:

Perfect score:

US-09-385-918-5 221 1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDDRLKIPA 38 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

2105692

length: 0 length: 2000000000 seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\* Database

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aab83020 Human Ned	Adb49217 Human WW	Aae32726 Human NED	Adq07991 Human NED	Aay25170 Human KIA	Aae32725 Human NED	Aau87973 Human WW	Adb49327 Novel hum	Aaw36797 Novel hum	Adb49320 Novel hum		Adq97134 Human can	Aau77715 Diseased	Abp58332 Human cel	Adb75453 Prostate	Adb75455 Prostate	Abg01080 Novel hum	Adr66480 Human pro	Adr66138 Human pro	Human	Ado55161 Protein #	Adq97125 Mouse can	Adq07990 Human NED	Human	Aaw93167 Human ZGG
	ID	AAB83020	ADB49217	AAE32726	ADQ07991	AAY25170	AAE32725	AAU87973	ADB49327	AAW36797	ADB49320	AAW13386	ADQ97134	AAU77715	ABP58332	ADB75453	ADB75455	ABG01080	ADR66480	ADR66138	ADQ97130	ADO55161	ADQ97125	ADQ07990	ADQ97128	AAW93167
	DB	4	7	9	æ	7	9	Ŋ	7	~	7	~	æ	ß	9	7	7	4	œ	æ	æ	œ	ω	α	œ	~
	Length	38	38	733	900	927	927	38	38	724	725	818	830	834	854	854	911	923	940	940	941	948	954	955	958	975
مه ان م	_	100.0	100.0	100.0	100.0	100.0	100.0	84.6	84.6	84.6	84.6	84.6	84.6	84.6		84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6
	Score	221	221	221	221	221	221	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187
Regult	NO.	1	7	m	4	'n	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aae32719 KIAA0439	Adb75451 Prostate	Ade60011 Human Pro	Human	Adr04136 Human Ned	Adq97132 Human can	Abg11772 Novel hum	Aau87962 Human WW			Abj26104 Aspergill	Yeast	Aab83023 Yeast Rsp	Adb49216 Yeast WW	Aaw13385 Human pro	Abp73459 Candida a	Abb63355 Drosophil	Aar97685 Yeast Rsp	Aaw37636 Peptide c	Aab83024 Yeast Rsp
AAE32719	ADB75451	ADE60011	ADD45762	ADR04136	ADQ97132	ABG11772	AAU87962	ADB49322	ABJ25504	ABJ26104	AAR97684	AAB83023	ADB49216	AAW13385	ABP73459	ABB63355	AAR97685	AAW37636	AAB83024
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995	995	995	995	995	1000	101	38	56	759	869	38	38	38	166	832	1082	38	38	38
84.6	84.6	84.6	84.6	84.6	84.6	84.6	67.4	65.2	64.3	64.3	61.5	61.5	61.5	61.5	61.5	9.09	59.3	59.3	59.3
187	187	187	187	187	187	187	149	144	142	142	136	136	136	136	136	134	131	131	131
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; WW domain; Nedd4. Human Nedd4 HECT E3 ubiquitin ligase WW domain #3. AAB83020 standard; peptide; 38 AA 29-AUG-2000; 2000WO-US023729. 99US-00385918. 25-JUN-2001 (first entry) WO200116604-A1. Homo sapiens. 30-AUG-1999; 08-MAR-2001. AAB83020; AAB83020 

(SIGN-) SIGNAL PHARM INC.

Murray BW, Hoekstra MF, Xie W,

Mercurio FM;

WPI; 2001-327913/34.

Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.

Disclosure; Page 13; 75pp; English.

The present sequence is the WW domain of a HECT (homologous to E6 carboxyl terminus) B3 ubiquitin ligase. The WW domain binds to the Smad Py motif, resulting in ubiquitinalion of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad Py motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein

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                             bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating troken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
ubiquitin ligase activity. The method is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain; drug candidate screening; drug discovery; drug modification; ig refinement; immunogen; WW binding protein; human; ned4; WW domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 221; DB 4; 100.0%; Pred. No. 2.2e-22; ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 38; Conservative
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(FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pirozzi G, Kay BK,
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                                                                                                                                                                                                                                                                                                                                                      Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-APR-1997;
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               activities, or as an immunogen to generate antibodies. This is the amino acid sequence of WW binding protein Ned4 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                     Viral infection; lymphosarcoma; human immunodeficiency virus; hepatitis; poliomyelitis; HIV; measles; protein therapy; human; NEDD4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein complex comprising HECT-RCC1, viral maturation scaffolding protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles, or BDola.
                                                                                                                                   Gaps
for discovering polypeptides involved in pharmacological
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                                                                                                   Length 38;
                                                                                                                                   Indels
                                                                                                                                                                                    GFLPKGWEVRHAPNGRPFIDHNTKTTTWEDPRLKIPA 38
                                                                                                ; Score 221; DB 7;
; Pred. No. 2.2e-22;
0; Mismatches 0;
                                                                                                                                                                    1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 16; 150pp; English.
                                                                                                                                                                                                                                                                                    AAE32726 standard; protein; 733
                                                                                                                                                                                                                                                                                                                                                                                      Human NEDD4 short form protein.
                                                                                                 100.0%;
100.0%;
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31-JUL-2001; 2001US-0308958P.
07-DEC-2001; 2001US-0340170P.
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                                                                                     Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                  Sequence 38 AA;
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 refinement,
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                                                                                                                                                                                                                                                                                                                       AAE32726;
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                                                                                                                                                                                                                                                      RESULT 3
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                             RESULT 5
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pathway modulating agent or for modulating a beta-catenin pathway of a

cell. The invention also relates to a method of modulating a beta-catenin

pathway in a cell; and diagnosing a disease in a patient by detecting

pathway in a cell; and diagnosing a disease in a patient by detecting

mich a cell; and diagnosing a disease in a patient by detecting

cells. Beta-catenin (also known as Armadillo in Drosophila) plays a role

orthologues are able to modify the beta-catenin pathway in Drosophila

cells. Beta-catenin (also known as Armadillo in Drosophila) plays a role

in cell signalling via the Wingless (Wg)/Wnt signalling pathway which is

involved in cell cycle progression. Beta-catenin levels are tightly

regulated by a complex containing the tumour suppressor proteins APC

(adenomatous polyposis coli) and Axin and the serine/threonine kinase

contained by a complex containing the tumour suppressor proteins APC

(adenomatous polyposis coli) and Axin and the serine/threonine kinase

contained by a complex containing the tumour suppressor proteins APC

(adenomatous polyposis coli) and Axin and the serine/threonine kinase

contained by a complex containing the tendent accumulates in

the induction of target genes such as the cell-cycle regulators cyclin DI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for diagnosing and treating cancer, comprises providing an assay system comprising a MBCAT polypeptide or nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                          MBCAT; modifier of beta-catenin; drug screening; beta-catenin pathway; beta-catenin pathway modulator; Wingless signalling pathway; Will signalling pathway; call cycle progression; diagnosis; cancer; angiogenic disorder; apoptotic disorder; coll proliferation disorder; cytostatic; gene therapy; human; NEDD4; neural precursor cell expressed developmentally downregulated 4.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a candidate beta-catenin MBCAT pathway modulating agent,
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                                                                   Length 733;
                                                                                                  0; Indels
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                                                                                                                                                         Score 221; DB 6;
Pred. No. 6.7e-21;
; Mismatches 0;
                                                                                                                                    1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA
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                                                                                                                                                                                                                                                        ADQ07991 standard; protein; 900 AA
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                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFSEQ; XM 046129.4.
                                                                                                                                                                                                                                                                                                                                                              Human NEDD4 protein.
                                                                Query Match
Best Local Similarity
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                                Sequence 733 AA;
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invention
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                                                                                                  Matches
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Inhibitor; ubiquitin-mediated proteolysis; IkappaB polypeptide; HECT; ubiquitin-conjugating system; Homologous to E6-Ap carboxyl terminus; lubiquitin-conjugating system; Homologous to E6-Ap carboxyl terminus; ubiquitin, ubiquitination; RSC ligase; KIAAN ligase; UBC4; MAD3; modulator; treatment; proliferative disorder; apoptosis; sepsis; differentiative disorder; viral infection; tissue wasting disorder; cachexia; malignancy; inflammatory disease; parasitic disease; tuberculosis; IL-2 therapy; rheumatory disease; parasitic disease; cerebral malaria; gouty arthritis; respiratory distress syndrome; cerebral malaria; chronic pulmonary inflammatory disease; silicosis; pulmonary sarcoidosis; bone resorption disease; reperfusion injury; graft versus host reaction; allograft rejection; Crohn's disease; systemic lupus erythematosus; leprosy; AIDS.
                    as
defective or impaired beta-catenin function and/or MBCAT function such cancer, or angiogenic, apoptotic or cell proliferation disorders. Proteins that interact with MBCAT are also useful in detecting and providing information about the function of MBCAT proteins. The present sequence represents a human NBDP4 (neural precursor cell expressed developmentally downregulated 4) protein, identified as an MBCAT polypeptide in an example of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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products for treating e.g. proliferative and/or differentiative
disorders, infections, tissue wasting, cachexia or AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 221; DB 8; Best Local Similarity 100.0%; Pred. No. 8.5e-21; Matches 38; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human KIAAN ligase protein fragment.
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N-PSDB; AAX78494.
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                                                                                                                                                                                                                                                                                                                                    Sequence 900 AA;
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Igase and ubiquitin, to promote ubiquitination of the Ikappas polypeptide by the HECT ligase; (b) contacting the ubiquitination of ubiquitinin, to promote ubiquitination of the Ikappas a level of ubiquitination of the candidate agent, (c) measuring a level of ubiquitination of the candidate agent, where a statisfically significant decrease in the absence of the candidate agent; where a statisfically significant decrease in ubiquitination of tha Ikappas polypeptide in the absence of the candidate agent; where a statisfically significant decrease in ubiquitination of tha Ikappas polypeptide in the presence of the candidate agent; where a statisfically significant decrease in ubiquitination of tha Ikappas polypeptide in the presence of the candidate agent; so that Ikappas polypeptide in the presence of the candidate agent is indicative of an inhibitor of ubiquitination of the Candidate agent is indicative of an inhibitor of ubiquitination of the companies of conviral states and or a upiquitination of an Ikappas (or other cellular or viral substrate) by a HECT ligase, such as RSC or KIAAN. Such modulate binding and/or ubiquitinylation of an Ikappas (or other cellular or viral infections, and in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, in the treatment of cachexia secondary to infection or malignancy, cachexia secondary to infection or malignancy, cachexia secondary to infection are malignancy, cachexia secondary to infection are arthritis, or sepsis, reperfusion injury, graft versus fost reaction, allograft rejections, crobn's disease, ulcerative colitis, or pyresis, in the creatment of autoimmune diseases such as multiple sclerosis, autoimmune diseases such as multiple sclerosis, autoimmune diseases such as multiple sclerosis, autoimmune clabetes, systemic lupus erythematosus; and ENL in leprosy, HIV, and the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral infection, lymphosarcoma, human immunodeficiency virus, hepatitis, poliomyelitis, HIV, measles, protein therapy, human, NEDD4.
[kappaB polypeptide and a HECT (Homologous to E6-Ap Carboxyl Terminus)
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/note= "HECT domain"
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/note= "WW domain"
821. .923
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31-JUL-2001; 2001US-0308958P.
07-DEC-2001; 2001US-0340170P.
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Best Local Similarity 100.
Matches 38; Conservative
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The invention relates to a method for modulation of viral maturation. The invention also provides an isolated protein complex comprising a HECT-RCC1 selected from HETT-WW, HECT-RCC1, Gag protein, Gag late domain, Pl3, actin, myosin, HSp60, HSp70, HSp90, STAM1, STAM2A, STAM2B, VMS-UIM, GTPBSe, E2 enzyme, tsg101, cullin, HERC1, HERC2, HERC3, Nedd4 -like protein or clathrin. The complexes, proteins, antibodies and methods are useful for treating viral infections, such as lymphosarcoma, human immunodeficiency virus (HIV), hepatitis, poliomyelitis, messles, or Ebola and for inhibiting budding in a subject. They are also useful in diagnostic assays for determining whether a cell is infected with a virus and for characterising the nature, progression and/or infectivity of the infection is also useful in protein therapy. The present sequence is human NEDD4 protein used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PDZ domain, WW domain, rat, cow, mouse, fruitfly, protein therapy, gene therapy, PDZ-mediated disease, inward potassium channel, WBP; dimer inhibitor peptide, carboxylate binding loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methods for identifying polypeptides comprising PDZ domains, the polypeptides and their encoding nucleic acids, useful for the diagnosis and treatment of PDZ related disorders.
                                                                                                                                                               New protein complex comprising HECT-RCC1, viral maturation scaffolding protein (VMSP), and/or HIV gag protein, useful for treating viral infections, such lymphosarcoma, HIV, hepatitis, poliomyelitis, measles, or Bbola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Alroy I;
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Reiss Y,
                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 15; 150pp; English.
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Greener T, Moskowitz H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pirozzi G,
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                                                                 WPI; 2003-111976/10.
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Matches 38; Conserv
                                                                                                 N-PSDB; AAD50459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 927 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200207751-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         misc
                                                                                                                                                                                                      RESULT 9
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                                                                                                                                                                                                                   AAW36797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 681, 906, 224 or 725 amino acids fully defined in the specification. (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (I) with the
                   The invention relates to methods for identifying polypeptides comprising PDZ domains, and their encoding nucleic acids. The sequences are used to identify modulators of their expression, function and activity, for use in the diagnosis and treatment of PDZ related disorders. Antibodies against the proteins and cells that produce them may be used for the treatment of PDZ-mediated disease states. Sequences AANBT843-AANB7974 represent proteins containing PDZ domains, fragments of these proteins and other related peptides used in the methods of the invention
                                                                                                                                                                                                                                                                                                                                                                                                           WW domain; drug candidate screening; drug discovery; drug modification;
drug refinement; immunogen; WW binding protein 4; WWP4; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                                                                                                                                                                                        Gaps
                                                                                                                                                                                          ö
                                                                                                                                                                 Length 38;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 37
                                                                                                                                                                                                                2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                               84.6%; Score 187; DB 5;
88.9%; Pred. No. 8.8e-18;
ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                 Novel human WWP4-2 protein WW domain.
Disclosure; Fig 20; 225pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fowlkes DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 5; 133pp; English.
                                                                                                                                                                                                                                                                                                      ADB49327 standard; peptide; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUN-2002; 2002US-00185050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00630916.
97US-00826516.
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                           Best Local Similarity 88.9
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIROZZI G.
KAY B K.
FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-635075/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003077577-A1.
                                                                                                                                         Sequence 38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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03-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibodies.
                                                                                                                                                                                                                                                                                                                                 ADB49327;
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PIRO/) (KAYB/) (FOWL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pirozzi
                                                                                                                                                                                                                                                                              RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide recognition unit, YAP WW domain binding protein, WBP-1; WBP-2; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; WWP4.
recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate antibodies. This is the amino acid sequence of novel human WW binding protein WWP4-2 WW domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "the nucleotides encoding these amino acids are
                                                                                                                                                                                                                                                                  Gaps.
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                                                                                                                                                                                                         Length 38;
                                                                                                                                                                                                                                                                  Indels
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140. 165
/note= "claimed (claim 49) WW Domain 1"
252. 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "claimed (claim 90) HECT domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "claimed (claim 49) WW domain
                                                                                                                                                                                                                                                                                                                                                          2 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 37
                                                                                                                                                                                                                                                                                                                     2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                      Score 187; DB 7;
Pred. No. 8.8e-18;
L; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human gene, designated WWP4.
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                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36797 standard; peptide; 724
                                                                                                                                                                                                         84.6%;
88.9%;
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(UYNC-) UNIV NORTH CAROLINA.
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                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                   Sequence 38 AA;
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contact with at least one recognition unit having a selective affinity

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number of proteins from a variety of species including humans, nematodes and yeast. Its name is derived from the observation that two tryptophan residues, one in the anno terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domains have a function involving cell signalling and growth regulation or the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many polypeptides and identifying those with selective affinity for the complex. Proteins containing WW domain ser used for targeted drug screening, i.e. to identify potential modulators of specific WW domain interactions. The valency of the recognition unit is important in form and the containing specificity of interaction with WW domain and the containing specificity of interaction with WW domain and the containing specificity of interaction with WW domains and the containing specificity of interaction with WW domains and the containing specificity of interaction with WW domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      form specificity is relaxed, but not lost, so proteins containing WW domains similar, but not identical, to the sequence of the peptides' target WW can be detected, including new polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                            Score 187; DB 2; Length 724;
Pred. No. 2.6e-16;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human WWP (WW binding protein) 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain; drug candidate screening;
ug refinement; immunogen; WWP4; WW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 69; Fig 23; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB49320 standard; protein; 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fowlkes DM;
                                                                                                                                                                                                                                                                                                                                                                                              84.6%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 88.2
Best Local 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAYB/) KAY B K.
(FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pirozzi G, Kay BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-635075/60
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KAY B K.
                                                                                                                                                                                                                                                                                                                                                        Sequence 724 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-APR-1997;
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(KAYB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug
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           for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of the arctifing when brought into contact with one another in the absence of the drug candidate, and determining the effect, if any of the presence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate antibodies. This is the amino acid sequence of a novel human WW binding protein WWP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human and Saccharomyces pombe protein ubiquitin ligase(s) - involved in cdc25 phosphatase and p53 ubiquitination, and regulate cell growth and
                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein ubiquitin ligase, pub2, cdc25 phosphatase, CDK kinase, cell cycle, transgenic animal.
                                                                                                                                                                                                                                  Length 725;
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                                                                                                                                                                                                                                                                                                                                           FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 283
                                                                                                                                                                                                                                                                                                       FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                  Score 187; DB 7;
Pred. No. 2.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein ubiquitin ligase pub3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 87-91; 108pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COLD-) COLD SPRING HARBOR LAB
                                                                                                                                                                                                                                  84.6%;
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 32; Conservative
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                                                                                                                                                                                                Sequence 725 AA;
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WPI; 2002-257475/30.
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les 32; Conserv
                                                                                                                                            Munger WE,
                                                                                                                                                                        N-PSDB; ABK11668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 834 AA;
                                              WO200212439-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              the invention
                             Homo sapiens
                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP58332;
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                                                                                                                                            Sun H,
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treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kidney disease; nephrotropic; renal disease; IgA nephropathy; IgAN; asymptomatic microscopic haematuria; proteinuria; episodic gross haematuria; necrotising crescentic glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
           Gaps
                                                                                                                                                                                                                                                                                                                                              New isolated cancer associated nucleic acids comprising at least contiguous nucleotides, useful for diagnosing, preventing and/or cancers such as leukemia and lymphoma.
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                                                                                                                                                                       Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human.
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          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diseased kidney tissue associated novel human protein #2
                                                                                                                                                     Human cancer associated sequence HP4-08-005, SEQ ID 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 392
                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 187; DB 8;
88.9%; Pred. No. 3.1e-16;
                           2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP
Pred. No. 3e-1
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                            ADQ97134 standard; protein; 830 AA
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                                                                                                                                                                                                                                                                     27-DEC-2002; 2002US-00330773.
                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY INC.
88.98;
                                                                                                                                  (first entry)
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          Conservative
                                                                                                                                                                                                                                                                                                         Morris DW, Malandro MS;
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Local Similarity
                                                                                                                                                                                                             WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 830 AA;
                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                  07-OCT-2004
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                                                                                                               ADQ97134;
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Matches
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compound libraries to discover novel therapeutics to regulate kidney function, as an antigen to raise polyclonal or monoclonal antibodies, and as a therapeutic agent or target. Agents that modulate, up-or-down-regulate the expression of [11] or agents that agonise or antagonise the activity of the protein are useful to modulate biological and pathologic damage or end-stage renal disease (ESRD). This is the amino acid sequence of the diseased kidney associated novel human protein #2, described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed in diseased kidney tissue compared to normal kidney tissue. (1) and its encoded protein (II) are useful for diagnosing a renal disease state e.g. IgA nephropathy (IgAN) which presents as asymptomatic microscopic haematuria and/or proteinuria or episodic gross haematuria, necrotising crescentic glomerulonephritis (NCGN), minimal change disease (Min Ch) or renal hypertrophy (the cause of end-stage renal disease and early manifestation of diabetes), in a subject. (II) is useful; as a target for identifying agents which modulate the expression or activity of (I), for identifying binding partners, as novel target for screening synthetic small molecules and combinatorial or naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes that are differentially expressed in renal biopsy samples from patients with kidney diseases useful for diagnosing renal diseases such as IgA nephropathy or necrotizing crescentic glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an isolated nucleic acid molecule (I) that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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NCGN; minimal change disease; Min Ch; renal hypertrophy; diabetes; end-stage renal disease; ESRD; kidney function.
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Pred. No. 3.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001WO-US024635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0222731P
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Prostate; cancer; cytostatic; gene therapy; marker.

Prostate cancer marker protein.

04-DEC-2003

ADB75453 standard; protein; 854 AA.

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The present sequence is the protein sequence of human CGDD-3, a novel protein associated with cell growth, differentiation and death. The sequence is predicted from Incyte clone 366046CB1, which was isolated from a brain tumour tissue cell line cDNA library. Structural features establish the protein as being associated with cell growth, differentiation and death, with further evidence suggesting it to be a differentiatin protein ligase. The invention is based on novel human CGDD-1 to 21 proteins (see ABD58330-50), the polymucleotides encoding them (see ABZ4689-709), and to the use of these for the diagnosis, treatment or prevention of cell proliferative disorders including cancer, developmental disorders, neurological disorders, autoimmune disorders, reproductive disorders, and disorders of the placenta, and in the expression of proteins and nucleic acids associated with cell growth, and companies and mit cell growth,
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JN, Ding L, Elliott VS, Emerling BM, Gandhi AR;

JA, Hafalia AJA, Honchell CD, Lal PG, Lee SY;

Ramkumar J, Reddy R, Sanjanwala MM, Tang YT;

Warren BA, Xu Y, Yang J, Yao MG, Yue H;
neuroleptic, tranquillizer, immunosuppressive, anti-HIV; antiallergic, antiasthmatic; antithyroid; antidiabetic; dermatological; nephrotropic; antiathematic; antiathritic; antialers; vulnesray; virucide; antibacterial; fungicide; antiparasitic; protozoacide; antihelminthic; antinifertility; gynaecological; ubiquitin protein ligase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human proteins associated with cell growth, differentiation and death, useful for treating, diagnosing or preventing cancer, developmental, neurological, reproductive or autoimmune/inflammatory
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88.9%; Pred. No. 3.2e-16;
ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                           10-AFR-2001; 20010S-0283294P.
26-AFR-2001; 20010S-0286230F.
27-AFR-2001; 20010S-028728F.
16-MAY-2001; 20010S-0291662P.
18-MAY-2001; 20010S-0291846P.
25-MAY-2001; 20010S-029372P.
01-UNA-2001; 20010S-0295340P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001; 2001US-0295340P.
15-JAN-2002; 2002US-0349705P.
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Best Local Similarity 88.9
Matches 32; Conservative
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Borowsky ML, Burford N,
Gietzen KJ, Griffin JA,
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N-PSDB; ABZ24691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zebarjadian Y;
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                           05-APR-2002;
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                                                                                                      gene therapy
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New nucleic acid molecule, useful for diagnosing or treating prostate

Disclosure; SEQ ID NO 277; 99pp; English

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Gorbatcheva Anderson D;

WO, Gannavarapu M, M, Glatt K, Zhao X,

Wonsey AM, Endege

Monahan JE, I R, Monares S, Kamatkar S, V

Hoersh S, Schlegel

WPI; 2003-248033/24.

, 2001US-0307982P. ; 2001US-0314356P. ; 2001US-0325020P. ; 2001US-0341746P. ; 2002US-0362158P.

(MILL-) MILLENNIUM PHARM INC.

25-JUL-2002; 2002WO-US023913.

25-JUL-2001; 22-AUG-2001; 25-SEP-2001; 12-DEC-2001; 05-MAR-2002;

WO2003009814-A2

06-FEB-2003

Homo sapiens

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The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control non-prostate cancer in the patient sample and the normal sevel indicates that the patient is afflicted with prostate cancer.

Nucleic acacca, and may be useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75611 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but
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88.9%; Pred. No. 3.2e-16;
iive 1; Mismatches
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Best Local Similarity 88.99
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Gaps ö

FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 412 2 FLPKGWEVRHAPNGRPFIDHNTKTTTWEDPRLKIP 37

377

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TYPE: amino acid STRANDEDNESS:
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43942, A
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                                                       October 13, 2005, 13:50:53; Search time 18.0952 Seconds (without alignments) 156.763 Million cell updates/sec
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Sequence 4, Ap
Sequence 22, A
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Sequence
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                                                                                            US-09-385-918-5
221
1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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S-08-630-916A-50
S-09-949-016-8946
S-09-248-796A-18187
S-08-630-916A-24
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US-08-935-601-6

US-08-533-205A-6

US-08-532-163A-4

US-08-530-205A-4

US-08-30-916A-22

US-08-30-916A-22

US-08-30-916A-22

US-08-476-509B-17

US-08-770-767-89345

US-09-270-767-43942

US-08-44-312-4

US-08-630-916A-36

US-08-630-916A-48

US-08-44-312-2

US-08-44-312-2

US-08-44-312-2

US-08-44-312-2

US-08-630-916A-46

US-08-630-916A-46

US-08-630-916A-46

US-08-630-916A-46

US-08-630-916A-36

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US-08-630-916A-36

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US-08-630-916A-36
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                513545 segs, 74649064 residues
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                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     protein search, using sw model
                                                                                                                                                Gapop 10.0 , Gapext 0.5
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No.
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APPLICANT: PIOZZI, Gregorio
APPLICANT: PIOZZI, Gregorio
APPLICANT: FWINCAI, Brian K.
APPLICANT: FWINCAIN INDINARY, BRIAN K.
APPLICANT: FOWINCAIN IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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                           Sequence 31, App
Sequence 33, Appli
Sequence 3, Appli
Sequence 4, Appli
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Sequence 2, Appli
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Sequence 25, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 37, Appli
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Sequence 5, At
Sequence 5, At
Sequence 37, A
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            US-08-476-509B-15
US-09-774-639-371
US-09-770-060-3
US-09-357-746-3
US-09-357-746-4
US-09-357-746-4
US-08-530-916A-2
US-08-630-916A-2
US-08-630-916A-35
                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 43.5
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 896-8864/9741
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-630-916A-23; Sequence 23, Application US/08630916A; Sequence 13, Application US/08630916A; Setent No. 6011137; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: United States
ZIP: 10036-2711
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Best Local Similarity 100.
Matches 38; Conservative
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
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COUNTRY: USA
ZIP: 02109-2170
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US-09-392-163A-6
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; Sequence 6, Application US/08539205A
; Patent No. 6001619
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
; TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Sequence 6, Application US/08895601

Sequence 6, Application US/08895601

Patent No. 606026

GENERAL INFORMATION:

APPLICANT: Beer-Romero, Peggy
APPLICANT: Strack, Peter J.

APPLICANT: Glass, Susan J.

TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,

TITLE OF INVENTION: REGULATION OF KAPPA B (IKB) DEGRADATION,

TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE:

ADDRESSE: FOLEY, MOGG & ELLOT LLP

STREET: One Post Office Square

CITY: Boston

STARTET.
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 02109-2170

COMPUTER READBLE FORM:
MEDIUM YYPE: FILPOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-BEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,601
FILING DATE: 16-0110-1997
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: MIV-096.01
TELECHONE: 617-832-1000
TELEFAX: 617-832-1000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-601-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CILL.
STATE: MA
COUNTRY: USA
TO: 02109-2170
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SOFTWARE PARENTIN Release #1.0, Version #1.30

CURRENT ACTUALION NUMBER: US/05/519,205A

FILIND DATE: 04-COT-1959

ATUDING DATE: 04-COT-1959

TELECOMMULATION NUMBER: CSV-005.01

TELECOMMULATION NUMBER: CSV-005.01

TELECOMMULATION NUMBER: CSV-005.01

TELECOMMULATION NUMBER: 05-000

INDOMESTICATION NUMBER: 05-000

INDOMESTICATION NUMBER: 05-000

ATUDING DATE: 0
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-392-163A-4

Sequence 4, Application US/09392163A

Sequence 4, Application US/09392163A

Patent No. 6503742

GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Netfery, Bradley

TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6

NUMBER OF SEQUENCES: 6

SORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
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      Length 834;
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                                                 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/539,205A

FILING DATE: 04-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REFERENCE/DOCKET NUMBER: 36,709

REFERENCE/DOCKET NUMBER: 36,709

REFERENCE/DOCKET NUMBER: 36,709

TELEPHONE: (617) 832-1000

TELEPHONE: (617) 832-1000
                                                                                                               357 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDDRLKFP 392
                                                                                        2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
  Score 187; DB 4;
Pred. No. 1.8e-17;
1; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 66.1%; Score 146; DB 3; Local Similarity 69.7%; Pred. No. 8.16-12; nes 23; Conservative 4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 GELPPGWEQRYTPEGRPYFVDHNTRTTTWVDPR 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                   US-08-539-205A-4; Sequence 4, Application US/08539205A; Patent No. 6001619
Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-539-205A-4
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STREET: Chr
THY: BOSTON
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USA
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STATE: MA
COUNTRY:
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Matches
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NGS-08-630-916A-22

| Sequence 22, Application US/08630916A
| Sequence 22, Application US/08630916A
| Sequence 22, Application US/08630916A
| Sequence 22, Application College College
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COUNTRY: United States
CONDUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 GELPPGWEQRYTPEGRPYFVDHNTRTTTWVDPR 320
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/539,205
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-7000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 766 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-09-392-163A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 23; Conserv
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A SH2 DOMAIN ASSOCIATED PROTEIN, A SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE SIGNALLING AND THE DOMAIN, AND DIAGNOSTIC AND THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59345, Application US/09270767

Batent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 187-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%; Score 136; DB 3;
66.7%; Pred. No. 5.8e-12;
tive 3; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
    1 GELPSGWEQRFTPEGRAYFVDHNTRTTWVDPR 33
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                                                                                                  Sequence 17, Application US/08476509B
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 I
TITLE OF INVENTION: PROTEIT
TITLE OF INVENTION: PROTEIT
TITLE OF INVENTION: PROTEIT
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 13521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
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Best Local Similarity 66...
Best Local Similarity 66...
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                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Yeas
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: 1
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-270-767-59345
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                                                                                         US-08-476-509B-17
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TELEX: 13
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Batent No. 602240

GENERAL INFORMATION:

APPLICANT: SUDOL, MARIUS

APPLICANT: HENRY, CHEN

TITLE OF INVENTION: A SIC DOMAIN ASSOCIATED PROTEIN, A

TITLE OF INVENTION: PROTEIN AND THE DOMAIN, THEREIN, NUCLEIC ACIDS ENCODING THE

TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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                                                                                                                                                     Score 136; DB 3; Length 38;
Pred. No. 5.8e-12;
3; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: 01-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%; Score 136; DB 3;
ilarity 66.7%; Pred. No. 5.8e-12;
Conservative 3; Mismatches 8.
                                                                                                                                                                                                                                                                1 GELPSGWEORFTPEGRAYFVDHNTRTTTWVDPR 33
                                                                                                                                                                                                                                          1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
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STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201343-1684
TELEX: 133521
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHRACTERISTICS:
LENGTH: 38 amino acids
  LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07601
                                                                                                                                                                                                                                                                                                                                                                       US-08-348-518C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-348-518C-17
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LENGTH:
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REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 64...
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 38 amino acids
                                                                                                                                                                                                   MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 21;
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Patent No. 5948639
EREAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5948639el TGF-{SYMBOL 98 \f "Symbol"} Pathway Genes NUMBER OF SEQUENCES: 16
CORRESSONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FISCHERCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43942
LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.6%; Score 134; DB 4; Length 435; llarity 64.9%; Pred. No. 1.9e-10; Conservative 4; Mismatches 9; Indels
                                                                                                                                           Score 134; DB 4; Length Low Pred, No. 5.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDPRLSNP 145
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

GURRENT APPLICATION NATR:

APPLICATION NUMBER: US/08/844,312
                                                                                                                                                                                                                                                                   55 GPLPEGWEERVHTDGRVFYIDHNTRTTQWEDPRLSNP 91
                                                                                                                                                                                                                                            1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-270-767-43942
US-09-evence 43942, Application US/09270767
Petent No. 6703491
                                                                                ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-59345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Drosophila melanogaster
US-09-270-767-43942
                                                                                                                                                              64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
    NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59345
LENGTH: 158
                                                                                                                                                              Query Match 60.6
Best Local Similarity 64.9
Matches 24; Conservative
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STATE: Massachusetts
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
TITLE OF INVENTION: DENTHFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NOMBER OF SEQUENCES: 124
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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     Length 36;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
59.3%; Score 131; DB 2; ilarity 70.0%; Pred. No. 2.7e-11; Conservative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRL 34
                                                                                                                                    3 LPAGWEORELPNGRVYYVDHNTKTTTWERP 32
                                                                                                       3 LPKGWEVRHAPNGRPFFIDHNTKTTTWEDP 32
                                                                                                                                                                                                                                                              US-08-630-916A-26; Sequence 26, Application US/08630916A; Sequence 26, Application US/08630916A; Setent No. 6011137; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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protein
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-348-518C-18
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APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                    Sequence 34, Application US/08630916A
| Sequence 34, Application US/08630916A
| Patent No. 6011137 |
| GENERAL INFORMATION: |
| APPLICANT: Pirozzi, Gregorio |
| APPLICANT: Fowlkes, Dana M. |
| TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL |
| TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME |
| NUMBER OF SEQUENCES: 124 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Pennie & Edmonds |
| STREET: New York |
| CITY: New York |
| COMMINSION |
| COMMIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUNTRY: New York
CUUNTRY: United States
ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FLING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 1101-203
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 396-8664/941
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
MENDETHE AND ACTION OF CHARACTERISTICS
MENDETHE AND ACTION OF SEQUENCE CHARACTERISTICS
MENDETHE AND ACTION OF SECUENCE CHARACTE
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Pred. No. 2.9e-11;
3; Mismatches 6;
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US-08-348-518C-18
Sequence 18, Application US/08348518C
; Patent No. 6022740
; GENERAL INFORMATION:
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Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klauber & Jackson
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Best Local Similarity 70.0°
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MOLECULE TYPE: peptide
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USA
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RESULT 14
US-08-630-916A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-630-916A-34
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COMPUTER: PADABLE PORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BW PC Compatible
CURRENT APPLICATION DATA:
COMPUTER: BALCADIE PAGE #1.0, Version #1.30

SOFTWARE: BALCATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,518C
FILING DATE: 0.10.EC-1994
CLASSIFFCATO: S14
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eeq. David A.
REGISTRATION NUMBER: & 600-1-101
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: All 3521
INFORMATION FOR SED ID NO: 18:
FEDEROMENTON FOR SED ID NO: 18:
CLOCHORY: As amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: NO COMPUTETION:
MEDITATE SOURCE:
COMPUTERIOL: NO
FRAGMENT TYPE: Internal
MEDITATE SOURCE:
COMPUTERIOL: NO
FRAGMENT TYPE: Asset-3
INMEDITATE SOURCE:
COMPUTERIOL: NO
FRAGMENT TYPE: A SOURCE:
COMPUTERIOL: NO
FRAGMENT TYPE: NO
FRAGMENT TYPE: A SOURCE:
COMPUTERIOL: NO
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October 13, 2005, 13:59:34; Search time 81.011 Seconds (without alignments) 195.471 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

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22: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1859788 seqs, 416717961 residues
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum Match
                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
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Maximum DB &
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 23, Appl	Sequence 5, Appli	16,	Sequence 15, Appl		169,	Sequence 126, App	Sequence 6, Appli	Sequence 277, App	Sequence 3, Appli	Sequence 3, Appli
SUMMARIES		ΩI	US-10-185-050-23	US-10-307-956-5	US-10-097-534-16	US-10-097-534-15	US-10-185-050-133	US-10-785-819-169	US-10-185-050-126	US-10-313-955-6	US-10-205-823-277	US-10-287-218-3	US-10-474-291-3
		DB	14	14	14	14	14	11	14	14	14	14	16
		Query Match Length DB ID	38	38	733	927	38	38	725	834	854	854	854
	æ	Query Match	100.0	100.0	100.0	100.0	84.6	84.6	84.6	84.6	84.6	84.6	84.6
		Score	221	221	221	221	187	187	187	187	187	187	187
		Result No.	1	7	٣	4	S	9	7	60	6	10	11

equence 277 equence 279 equence 279 equence 314	Sequence 97, Applia Sequence 275, Applia Sequence 42131, Applia Sequence 42131, Applia Sequence 158, Applia Sequen	# <b>#</b> m m 0; m		12, 216, 48, 134, 170,	Sequence 26, Appl Sequence 46, Appl Sequence 11, Appl Sequence 2, Appli Sequence 2, Appli Sequence 156, App
-11-051-454 -10-205-823 -11-051-454 -10-450-763	10-09/-53410-205-82311-051-45410-450-76310-785-819-	-10-313-955- -10-185-050- -10-128-714- -10-128-714- -10-185-050-	-10-032-585-7 -11-097-143-1 -10-185-050-2 -10-185-050-3 -10-307-956-9	-10-097-534 -10-723-860 -10-185-050 -10-185-050 -10-785-819	07-956-2 85-050-4 97-534-1 88-186-1 18-408-2 18-408-2
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## ALIGNMENTS

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TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRUT APPLICATION DATE: 28-Jun-2002
FILING DATE: 28-Jun-2002
CLASSIFICATION: ~Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
US-10-185-050-23
; Sequence 23, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
                                                                                             APPLICANT: Pirozzi, Gregorio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
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2

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TYPE: PRT
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Publication No. US20030049607A1

GENERAL INFORMATION:
APPLICANT: GREENER, TSVIKA
APPLICANT: MOSKOWITZ, HAIM
APPLICANT: ALROY, IRIS
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
TITLE OF INVENTION NUMBER: US/10/097, 534
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/275,224
PRIOR APPLICATION NUMBER: 60/308,958
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                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 38; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-097-534-16
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Sequence 133, Application US/10185050
Publication No. US2003007757741
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
Fewy, Brian K.
Fewy, Brian K.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: REISS, YUVAL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
TITLE OF INVENTION: MATURATION
FILE REPERENCE: PLV-001.01
CURRENT APPLICATION NUMBER: US/10/097,534
CURRENT APPLICATION NUMBER: US/275,224
PRIOR PELLON DATE: 2001-03-12
PRIOR PELLON APPLICATION NUMBER: 60/275,224
PRIOR PELLON APPLICATION NUMBER: 60/310, 170
PRIOR APPLICATION NUMBER: 60/310, 170
PRIOR PELLON DATE: 2001-07-31
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; Pred. No. 7.4e-20;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 100.0%; Score 221; DB 14; 100.0%; Pred. No. 5.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
PRIOR APPLICATION NUMBER: 60/340,170
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 733
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-10-097-534-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-097-534-15
Sequence 15, Application US/10097534
Publication No. US20030049607A1
GENERAL INFORMATION:
APPLICANT: GREENER, TSYIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 38; Conservative
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Homo sapiens
US-10-097-534-15
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Sequence 126, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caligiuri, Maureen
Nefsky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCES:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPOY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CIASSIFICATION: «Unknown>
PROPALICATION NUMBER: US/08/826,516
FILING DATE: 03-APF-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 118,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ 1D NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 725 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10313955
Publication No. US20030199036A1
GENERAL INFORMATION:
APPLICANT: Beach, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-185-050-126
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US-10-313-955-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: Herrero J
APPLICANT: Pirozzi, G.
APPLICANT: Uveges, A.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING PDZ DOMAINS AND METHODS OF USING SAME
FILE REFERENCE: 1101-211
CURRENT APPLICATION NUMBER: US/10/785,819
CURRENT FILING DATE: 2004-02-23
PRIOR APPLICATION NUMBER: US/09/723,810
PRIOR FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAMME: MESCOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.6%; Score 187; DB 14; Length 38;
88.9%; Pred. No. 6.2e-17;
iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 187; DB 17;
Pred. No. 6.2e-17;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: UAKNOWN

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-10-185-050-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 170
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 169, Application US/10785819; Publication No. US20050112552A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ 1D NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acida
TYPE: amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo Sapiens
US-10-785-819-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conserv
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; LENGTH: 854
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-277
     SEQ ID NO 277
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APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoerseft, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Pustin
APPLICANT: Anderson, Pustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, METHODS POR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: WTETAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/301,356
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR APPLICATION NUMBER: 60/314,746
PRIOR PLING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: 60/325,020
PRIOR PLING DATE: 2001-09-25
PRIOR PLING DATE: 2001-12-12
PRIOR PLING DATE: 2003-03-05
NUMBER OF SEQ ID NOS: 455
NUMBER OF SEQ ID NOS: 455
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88.9%; Pred. No. 1.8e-15;
tive 1; Mismatches 3; Indels (
                                                                      COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/313,955
FRING DATE: 05-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/392,163
FILING DATE: AUMRER: US 08/539,205
FILING DATE: AUMRER: US 08/539,205
FILING DATE: CUNKNOWN:
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                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-313-955-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 277, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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nes 32; Conservat
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APPLICANT: Anderson, Dustin

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION: TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

FILE REFERENCE: MRI-044

CURRENT APPLICATION NUMBER: US/10/205,823

PRIOR FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/307,982

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-07-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-12-12

PRIOR FILING DATE: 2001-12-12

PRIOR PLING DATE: 2001-12-12

PRIOR FILING DATE: 2001-12-12

PRIOR FILING DATE: 2001-12-12

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 455

SEQ ID NO 277

LENGITH: 854

***COFTWARE: FASESO FOR WINDOWS VERSION 4.0
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
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                                                                                                                                                                Sequence 277, Application US/11051454 Publication No. US20050191673A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gannavarapu, Manjula
Gorbatcheva, Bella
Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
                                                                                                                                                                                                                                                             APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John B.
APPLICANT: Bndege, Wilson O.
APPLICANT: Gannavazpu, Wanjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson
APPLICANT: Gannavarapu, Manji
APPLICANT: Gorbatcheva, Bell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-051-454-277
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                                                                                                                                     JS-11-051-454-277
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APPLICANT:
APPLICANT:
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APPLICANT: AZIMZAL, Yalda; AU-YOUNG, Janice K.
APPLICANT: BECHA, Sajeev; BAUGHN, Mariah R.
APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.
APPLICANT: BURFORD, Neil; DING, Li
APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
APPLICANT: GRIFFIN, Jennifer A.; HaFALLA, April J.A.
APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.
APPLICANT: HONCHELL, Cynthia D.; LAL, Machusudan M.
APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
APPLICANT: TANG, Y. Tom, CHWALA, Narinder K.
APPLICANT: XU, Yuning; YANG, Junming
APPLICANT: XU, Yuning; YANG, Junming
APPLICANT: ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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| CURRENT APPLICATION NUMBER: US/10/474,291
| CURRENT FILING DATE: 2003-10-06
| PRIOR PELING DATE: 2002-04-05
| PRIOR PELING DATE: 2002-04-05
| PRIOR PELING DATE: 2002-01-15
| PRIOR PELING DATE: 2001-06-01
| PRIOR PELING DATE: 2001-06-12
| PRIOR PELING DATE: 2001-06-13
| PRIOR PELING DATE: 2001-06-16
| PRIOR PELING DATE: 2001-04-26
| PRIOR PELING DATE: 2001-04-11
| PRIOR PELING DATE: PROGRAM
| PRIOR PELING DATE: 2001-04-11
| PRIOR PELING DATE: 2001-04-11
| PRIOR PELING DATE: PROGRAM
| PRIOR PELING DATE: 2001-04-11
| PRIOR PELING DATE: PROGRAM
| PRIOR PELING DATE: 2001-04-11
| PRIOR PELING DATE: PROGRAM
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                                  84.6%; Score 187; DB 14; Length 854;
Llarity, 88.9%; Pred. No. 1.8e-15;
Conservative 1; Mismatches 3; Indels (
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, OTHER INFORMATION: Incyte ID No: 3660046CD1
US-10-474-291-3
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10474291 Publication No. US20040132043A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PI-0417 USN
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Matches 32, Conservative
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Query Match
Best Local Similarity
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FEATURE:
NAME/KEY: DOMAIN
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US-10-450-763-31439
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                   Matches
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APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Ganter, Shubhangi
APPLICANT: Manetar Shubhangi
APPLICANT: Manderaon, Dustin
APPLICANT: Manderson, Dustin
APPLICANT: Anderson, METHODS FOR IDENTIFICATION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MI-044
CURRENT FLING DATE: 2005-02-04
FRIOR APPLICATION NUMBER: 05/10/205,823
FRIOR APPLICATION NUMBER: 60/310/205,823
FRIOR APPLICATION NUMBER: 60/310/205
FRIOR APPLICATION NUMBER: 60/314,356
FRIOR APPLICATION NUMBER: 60/315,020
FRIOR FILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: 60/315,020
FRIOR FILING DATE: 2001-10-22
FRIOR APPLICATION NUMBER: 60/315,020
FRIOR FILING DATE: 2001-10-22
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
NUMBER OF SEQ ID NOS: 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 187; DB 14
Pred. No. 2e-15;
1; Mismatches
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/310,982
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR PILING DATE: 2001-12-12
PRIOR PILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-05-5
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 279, Application US/11051454 Publication No. US20050191673A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Wonsey, Angela M.
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Homo sapiens
US-10-205-823-279
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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NAME/KEY: DOMAIN
LOCATION: (884)..(916)
OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: eMATRIX, accession number PF00632C, p-value=8.250e-26, raw score other information: 20.66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (6177...(922)
OTHER INFORMATION: HECT-domain (ubiquitin-transferase) domain identified by
OTHER INFORMATION: PFam, accession name HECT, E-value=1.6e-179, PFam score of 609.8
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84.6%; Score 187; DB 18; Length 923;
Best Local Similarity 88.9%; Pred. No. 2e-15;
Matches 32; Conservative 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                  GENERAL INVENTALIANOMI

GENERAL INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790C1P3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSCOM

LENGTH: 923
Indels
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i OTHER INFORMATION: Xaa = X or * as defined in Table
US-10-450-763-31439
3;
                                                                                 434 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 469
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                                                    2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: October 13, 2005, 14:50:01 Job time : 82.011 secs
                                                                                                                                                                                                                                            Sequence 31439, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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- protein search, using sw model OM protein Run on:

October 13, 2005, 14:36:01; Search time 15.8681 Seconds (without alignments) 230.414 Million cell updates/sec

US-09-385-918-5 221 1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ubiquitin-protein	ubiquitin-protein	ubiquitin-protein	probable ubiquitin	ubiquitin protein	ubiquitin-protein	brain-specific ang	NEDD-4 ORF - mouse	ubiquitin ligase N	hypothetical prote	hypothetical prote	probable guanylate	protein F13E6.4 (i	ø	synaptic scaffoldi	yes-associated pro		м	associat	domain-c	45K WW domain-cont	æ	dystrophin homolog	•	dystrophin - mouse	dystrophin, muscle	formin binding pro	Ω	
SUMMARIES	ID	T46412	566562	T37545	974	T39585	843217	JE0209	183196	S70642	T23160	T46292	T42372	G89632	T37900	T14152	B56954	150730	T47801	A56954	JC7507	JC7508	T33637	A41130	S02041	S28916	A27605	S64713	T25886	T20274
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	Query Match Length	820	166	767	815	786	809	1256	708	887	1012	616	1171	457	671	1277	472	448	1616	454	383	386	691	870	3660	3678	3685	67	241	889
de	Query Match	84.6	66.1	66.1	64.7	61.5	61.5	59.3	9.95	9.95	'n.	ů.	54.8	ω.	ä	ď	51.1	48.4	47.3	44.8	43.0	43.0	39.4	37.1	37.1	37.1	37.1	33.3	'n	32.4
	Score	187	146	146	143	136	136	131	125	125	123	121.5	121	118	115	115	113	0	104.5	66	95	95	87	82	82	82	82		72	71.5
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Pinl protein - hum peptidylprolyl iso hypotherical prote G-utrophin - mouse utrophin - human protein ZK1127.9 [ hypotherical ww do ESSI protein - yea hypothetical prote Pinl protein homol glycoprotein VP7 p	immune-responsive	artifact-warning s hypothetical prote
\$68520 JC7136 \$69038 184303 \$28331 \$28331 \$58094 \$552764 \$552764 \$56851 \$66851	154546 154546	E40201 T02117
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## ALIGNMENTS

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A) Accession: T46412
A) Accession: T46412
A) Status: preliminary
A) Accession: T46412
A) Status: preliminary
A) A) Status: preliminary
A) A) Status: preliminary
A) A) Status: preliminary
A) A) Coss-references: uNIPROT: Q9NT88; EMBL: AL137469
A) Cross-references: UNIPROT: Q9NT88; EMBL: AL137469
A) Coss-references: UNIPROT: Q9NT88; EMBL: AL1374222
C) Genetics:
A) Gene: GDB: NEDD4
A) Note: Drivzpd: A42422.1
A) A) Note: Drivzpd: A42422.1
C) Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquity C) C) C) C) C) Compain: WW repeat homology <WWR1>
F) A12-179/Domain: WW repeat homology <WWR2>
F) A342-379/Domain: WW repeat homology <WWR3>
F) A48-430/Domain: WW repeat homology <WWR3>
F) A89-814/Domain: ubiquitin-protein ligase homology <UBI>
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                               N;Alternate names: hypothetical protein DRFZp434P2422.1
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession T4641B.
S;Blum, H; Bauersachs, S; Mewes, H.W.; Gassenhuber, J; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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84.6%; Score 187; DB 2; Length 820;
Best Local Similarity 88.9%; Pred. No. 2.1e-16;
Matches 32; Conservative 1; Mismatches 3; Indels
ubiquitin-protein ligase (EC 6.3.2.19) NEDD4 - human (fragment)
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셤 ò

Uniquitin-protein ligase (EC 6.3.2.19) - fission yeast (Schizosaccharomyces pombe)
UNALternate names: E6-AP-like protein ubiquitin ligase
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Bate: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004
C;Accession: S66562; T45159
EMBO J. 15, 1301-1312, 1996
A;Title: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of cdc25
A;Reference number: S66562; MUID:96205868; PMID:8635463
A;Accession: S66562
A;Accession: S66562
A;Accession: S66562
A;Accession: S66563
A;Accession: S665

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;Cross-references: UNIPROT:014326; EMBL:Z99759; PIDN:CAB16903.1; GSPDB:GN00067; SPDB:SPP
                                                                                                                                                                                                                                           C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C;Accession: T4974
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ubiquitin-protein ligase (EC 6.3.2.19) RSP5 - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T39585
ubiquitin protein ligase - fission yeast (Schizosaccharomyces pombe)
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A;Experimental source: BAC clone B24B19; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 6
A;Introns: 11/1; 24/1; 59/2; 110/1; 783/2
C;Superfamily: yeast ubiquitin-protein ligase; WW repeat homology F;239-276.Domain: WW repeat homology <WWR1>
F;334-371/Domain: WW repeat homology <WWR2>
F;334-371/Domain: WW repeat homology <WWR2>
F;333-430/Domain: WW repeat homology <WWR3>
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                                                                                                                                                                               probable ubiquitin-protein ligase [imported] - Neurospora crassa
N/Alternate names: protein B24B19.160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 786;
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R;Volckaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G. Submitted to the EMBL Data Library, August 1997
A;Reference number: Z21865
A;Accession: T39585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.7%; Score 143; DB 2; Best Local Similarity 69.7%; Pred. No. 1.2e-10; Matches 23; Conservative 3; Mismatches 7
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Pred. No. 9.6e-10;
5; Mismatches 5
                288 GELPPGWEQRYTPEGRPYFVDHNTRTTTWVDPR 320
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
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Best Local Similarity 67.7%
Marches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: SPDB:SPBC16E9.11c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: T49744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
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A;Cross-references: UNIPROT:092462; EMBL:Z99161; PIDN:CAB16207.1; GSPDB:GN00066; SPDB:SF
A;Cross-references: UNIPROT:092462; EMBL:Z99161; PIDN:CAB16207.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h-; cosmid cl1G7
B;Saleki, R.; Jia, Z.; Karagiannis, J.; Young, P.G.
Mol. Gen. Genet. 254, 520-528, 1997
Mol. Gen. Genet. 254, 520-528, 1997
A;Title: Tolerance of low pH in Schizosaccharomyces pombe requires a functioning publ ub
A;Reference number: Z07985; MUID:97340937; PMID:9197411
submitted to the EMBL Data Library, August 1996
A;Description: Publ acts as an E6-AP-like protein ubiquitin ligase in the degradation of A;Reference number: Z22935
A;Reference number: Z22935
A;Accession: T45159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: L-766 <NE2>
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T37545

T37546

Midguitin-protein ligase (EC 6.3.2.19) publ [validated] - fission yeast (Schizosaccharom biguitin-protein ligase Publ
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: 31-Bec-1999 #sequence_revision 03-Bec-1999 #text_change 09-Jul-2004
C;Accession: T37545; T48655
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
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A;Description: EC 6.3.2.19 [validated, MUID:96205868]
C;Function: <CYC>
A;Description: involved in of the mitotic activating tyrosine phosphatase cdc25 [validat C;Function: <TOL>
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A;Experimental source: strain J227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                             C, Superfamily: yeast ubiquitin-protein ligase; WW repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.1%; Score 146; DB 1; Length 766; Best Local Similarity 69.7%; Pred. No. 4.6e-11; Matches 23; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 66.1%; Score 146; DB 2; Length 767; Similarity 69.7%; Pred. No. 4.6e-11; 23; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <SAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 GELPPGWEQRYTPEGRPYFVDHNTRTTTWVDPR 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
                                                                                                                                                                                                                                     A,Cross-references: EMBL:Y07592; PIDN:CAA68867.1
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: ligase
F;206-242/Domain: WW repeat homology <WW1>
F;288-325/Domain: WW repeat homology <WW2>
F;345-382/Domain: WW repeat homology <WW3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Keywords: cell cycle control; ligase F;205-242/Domain: WW repeat homology <WW1>F;208-25/Domain: WW repeat homology <WW2>F;345-382/Domain: WW repeat homology <WW3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: publ; SPDB:SPAC11G7.02
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A; Introns: 6/2; 14/1; 62/2
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Best Local S
Matches 23
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C,Accession: 18196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Biochem, Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression A;Reference number: 160167; MUID:92328780; PMID:1378265
A;Accession: 183196
A;Accession: 183196
A;Accession: Rinary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Gene: NEDD-4
C:Superfamily: rat ubiquitin-protein ligase, protein kinase C C2 region homology, ubiqui
F;40-77/Domain: WW repeat homology <WW1>
F;196-233/Domain: WW repeat homology <WW2>
F;251-288/Domain: WW repeat homology <WW3>
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A,Molecule type: mRNA
A,Residues: 1-887 <STA>
A,Cross-references: UNIPROT: Q62940; EMBL: U50842; NID: g1293646; PIDN: AAB48949.1; PID: g129
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C; Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiqui C; Superfamily: rat ubiquitin-protein kinase C C2 region homology «KC2>
F; 54-167 / Domain: protein kinase C C2 region homology «KC2>
F; 246-283 / Domain: WW repeat homology «WW1>
F; 402-439 / Domain: WW repeat homology «WW2>
F; 459-496 / Domain: WW repeat homology «WW3>
F; 555-881 / Domain: wipiquitin-protein ligase homology «UBI>
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R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.
EMBO J. 15, 2371-2380, 1996
A;Title: WW domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+)
A;Reference number: S70642; MUID:96221297; PMID:8665844
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb_1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LPKGWEVRHAPNGRPFFIDHNTKTTTW-----EDPRLKIPA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LPKGWEVRHAPNGRPFFIDHNTKTTTW-----EDPRLKIPA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;347-682/Domain: ubiquitin-protein ligase homology <UBI>
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A;Cross-references: GB:D10714; NID:g220508; PID:g220509
C;Genetics:
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                                                                                                                                                           300 GFLPENWEMAYTENGEVYFIDHNTKTTSWLDPR 332
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                                                                                                       1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR
                              Mismatches
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                              Conservative
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Best Local Similarity
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NiAlternate names: E6-AP-like protein ubiquitin ligase; protein YER125w; PUB1 protein C; Species: Saccharomoces cervainiae
C; Date: 10-Sep-1999 Hesquence_revision 10-Sep-1999 Hext_change 09-Jul-2004
R; Wulligan, J.T.: Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, A; Rocession: S43217
A; Molcocute to the EMBL Data Library, Pebruary 1993
A; Rocess-reference: UNIPROT: P39940; GB:U18916; EMBL:L11119; NID: G1384128; PIDN:AAC03223.
B; Pibietrich, F.S.
Submitted to the EMBL Data Library, December 1994
A; Possidues: 1-809 AULA
A; Rocession: S36628
A; Molcoute type: DNA
A; Rocession: S36628
A; Molcoute type: DNA
A; Rocession: S36628
A; Molcoute type: DNA
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Nalternate names: BAII-associated protein 1; BAPI [misnomer]
C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Date: 21-Aug-1998 #sequence_revision 247, 597-604, 1998
R;Shiratsuchi, T.; Futamura, M.; Oda, K.; Nishimori, H.; Nakamura, Y.; Tokino, T.
Biochem. Biophys. Res. Commun. 247, 597-604, 1998
A;Tille: Cloning and characterization of BAI-associated protein 1: A PDZ domain-containi
A;Reference number: JE0209
A;MUD:98321173; PMID:9647739
A;Accession: JE0209
A;MUD:98321173; PMID:9647739
A;Accession: JE0209
A;Accession:
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Pred. No. 7.5e-09;
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66.7%; Pred. No. 9.9e-10;
iive 3; Mismatches 8
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Matches 22; Conservative
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Best Local Similarity
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A,Title: Genome sequence of the nematode C. elegans: a platform for investigating biology, A,Reference number: A75000, MUID:99069613; PMID:9851916
A,Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q19404; GB:chr_X; PIDN:CAA92121.1; PID:g3875841; GSPDB:GN0005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Cross-references: UNIPROT:Q9UTG2; EMBL:AL117390; PIDN:CAB55856.1; GSPDB:GN00066; SPDB:6
A.Experimental source: strain 972h-; cosmid c1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ubiquitin-protein ligase - fission yeast (Schizosaccharomyces pombe) (Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Decies: Ob-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: T37900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein F13E6.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                     Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, September 1999
A;Reference number: Z21752
A;Accession: T37900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 GPLPAGWEMRLSEDYHVYFVDHSTKTTTWSDPRDNVVA 279
                                                    C;Keywords: alternative splicing; phosphotransferase F;330-337/Domain: WW repeat homology <WWR1>F;347-384/Domain: WW repeat homology <WWR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA
                                                                                                                                                                  Score 121; DB 2;
Pred. No. 1.4e-07;
5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 115; DB 2;
Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 118; DB 2; 57.6%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                            300 GPLPENWEMAYTENGEVYFIDHNTKTTSWLDPR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-671 <RIE>
                                                                                                                                                                                                                                                                                          33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.2e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                          1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LPKGWEVRHAPNGRPFIDHNTKTTTWEDPRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
A;Introns: 60/2; 105/1; 639/2
F;242-279/Domain: WW repeat homology <WWR>
                                                                                                                                                                     54.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.0%;
                                                                                                                                                                        Query Match
Best Local Similarity 60.6
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 57.6
Matches 19; Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-457 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: G89632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: G89632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: F13E6.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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                                                                                                                                                                                           A;Reference number: 219701
A;Accession: T23160
A;Residues: 1-1012 <WIL>
A;Residues: 1-1012 <WIL>
A;Cross-references: UNIPROT:Q21075; EMBL:Z68750; PIDN:CAA92965.1; GSPDB:GN00022; CESP:KG
A;Experimental source: clone K01A6
C;Genetics:
A;Gene: CESP:K01A6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable guanylate kinase (BC 2.7.4.8) 1, membrane-associated, splice form b - mouse C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: T42372
R; Dobrosotskaya, I; Guy, R.K; James, G.L.
A; Biol. Chem. 272, 31589-31597, 1997
A; Title: MAGI-1: a membrane-associated guanylate kinase with a unique arrangement of pro A; Reference number: Z22139; MUID:98058950; PMID:9395497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNÅ
A;Residues: 1-1171 cDOBA
A;Cross-references: UNIPROT:O54893; EMBL:AF027503; NID:g2702346; PID:g2702347; PIDN:AAB9
A;Experimental source: strain C57 Black/6 x CBA
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               hypothetical protein K01A6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23160
R;Cottage, A.
submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
T46292

hypothetical protein DKPZp434E0610.1 - human (fragment)
C;Speciaes: Homo sapiens (man)
C;Speciaes: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 15-Mar-2004
C;Accession: T46292
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
R;Duesternce number: Z23035
A;Accession: T46292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 107/1; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3
F;131-168/Domain: Ww repeat homology <WWR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.7%; Score 123; DB 2; Length 10 Best Local Similarity 60.6%; Pred. No. 6.5e-08; Matches 20; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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A;Cross-references: EMBL:AL137582
A;Experimental source: adult testis; clone DKFZp434E0610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.0%; Score 121.5; DB 2 60.6%; Pred. No. 5.8e-08; iive 6; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: T42372
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPR 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;62-100/Domain: WW repeat homology <WWR>
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Best Local Similarity 60.6
Matches 20; Conservative
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A;Note: DKF;
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RESULT 15
synaptic scaffolding protein S-SCAM - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Mar-2004
C;Date: 21-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 15-Mar-2004
C;Accession: T14152
R;Hits, A., i Hate, Y.; Ide, N.; Takeuchi, M.; Irie, M.; Yao, I.; Deguchi, M.; Toyoda, A.
J; Biol. Chem. 273, 21105-21110, 1998
A;Title: A novel multiple PDZ domain-containing molecule interacting with N-methyl-d-asp
A;Accession: T14152
A;Accession: T14152
A;Accession: T14152
A;Accession: T14154
A;Residues: 1-1277 <HIR>
A;Residues: 1-1277 <HIR>
A;Residues: 1-1277 <HIR>
A;Cossion: Treferences: EMBL:AF034863; NID:g3411052; PID:g3411053; PIDN:AAC31124.1
C;Genetics:
A;Gene: S-SCAM
C;Punction:
A;Description: may assemble receptors and cell adhesion proteins at synaptic junctions
F;302-339/Domain: WW repeat homology <WW2>
F;348-385/Domain: WW repeat homology <WW2>
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Search completed: October 13, 2005, 15:11:15 Job time : 15.8681 secs

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October 13, 2005, 14:03:23 ; Search time 72.381 Seconds (without alignments) 268.842 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
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268.842 Million cell ug Title: US-09-385-918-5 Perfect score: 221 Sequence: 1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	4 homo sapien	oryct			พนธ แ	pomod !	э рошо	mns mnscnin	0 mus musculu	mus m	homo /	homo	homo	homo			homo		xenol	2 schizosacch	5 neurospora	l neurospora		-		2 ashbya goss	6 schizosacch	0 saccharomyc	l candida gla		
Descr	P4693	Q9n134	Q8qgj	Q9nt 88	<b>Q8brt</b>	Q9h2w4	gebw5	099pk;	08cfi	0641n(	Q8n5a7	Q725£1	096pu5	Q7z5£2	042573	Q6gmd5	<b>07</b> z5n	043165	Q6dir6	092462	Q6m906	Q7rv01	<b>Q</b> 6c5h0	07ge76	Q9bkw4	<b>0</b> 75ai	01432	P3994	Q6fn7	Q6bt4	Q6cnc7
DI	NED4 HUMAN				QBBRT9			Q99PK2	QBCFIO			Q7Z5F1	Q96PUS	Q7Z5F2				043165		PUB1_SCHPO	Q6M9Q6	Q7RV01	Q6C5H0	Q7QE76	Q9BKW4		PUB3_SCHPO	RSP5_YEAST	Q6FN71	Q6BT41	Q6CNC7
DB	-	~	7	7	7	7	7	7	7	7	~	7	~	~	~	7	7	N	~	-			N	~	(1)	~	-	Н	~	7	~
Length	1000	455	571	820	835	854	852	852	855	875	911	947	955	196	971	971	975	995	970	767	787	806	854	917	724	817	α	809	822	781	819
% Query Match	100.0	~	4	4	84.6	4.	84.6	4.	84.6	84.6	4	4.	84.6		4	4	4	84.6	77.6	66.1	64.7	64.7	4	63.8	62.4	ď.	ä	61.5	ä	61.1	61.1
Score	221	215	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	187	171.5	146	143	143	142	141	138	138	n	136	136		135
Result No.	-	73	м	4		9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Q7pqr5 anopheles g Q7kur2 drosophila	Q95r64 drosophila											
Q7PQR5 Q7KUR2	Q95R64	Q95TQ0	Q8IQR6	Q9VVI3	WWP2 HUMAN	WWP2 MOUSE	NED4_MOUSE	NED4_RAT	WWP1 MOUSE	WWP1_HUMAN	Q7PW66	Q9BWY0
793 2	334 2	338 2	356 2	07 2	370 1	370 1	187 1	187 1	118 1	122 1	945 2	108 2
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61.1	. 09	90.	. 09	.09	59.	59.	. 96	56.	.96	56.	56.	55.
135	134	134	134	134	131	131	125	125	124	124	124	123
33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Gaps

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increases the related to the Nedd4 family of ubiquitin protein ligases increact with the L domain of Rous sarcoma virus and are required for gag budding from cells.";

Proc. Natl. Acad. Sci. U.S.A. 98:11199-11204(2001).

-! -SIMILARITY: Contains 1 C2 domain.

HSSP; 052940; 115H.

INTERPRO; ITRN000008; C2.

INTERPRO; IPRN000349; WW.

InterPro; IPRN0120349; WW.

Fram; PRO0120; WW.RSP5_WWP.

Pfam; PRO0120; WW.RSP5_WWP.
                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21457266; PubMed=11562473; DOI=10.1073/pnas.201268998;
Kikonyogo A., Bouamr F., Vana M.L., Xiang Y., Aiyar A., Carter C.,
                                                     Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 571;
                                                   97.3%; Score 215; DB 2; Length 45 ilarity 97.4%; Pred. No. 3.5e-19; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                  51811 MW; D1C4549B52E22298 CRC64;
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                                                                                                                                                  329 GFLPKGWEVRHAPNGSPFFIDHNTKTTTWEDPRLKIPA 366
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp434P2422 (Fragment).
                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Late domain-interacting protein 1 (Fragment).
                                                                                                                             1 GFLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIPA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 187; DB 2;
88.9%; Pred. No. 1.7e-15;
iive 1; Mismatches 3;
                                                                                                                                                                                                                                                          571 AA
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PRINTS; PR00403; WWDOMAIN.
SMART; SM00239; C2; 1.
SMART; SM00456; WW; 4.
PROSITE; PS00499; C2_DOMAIN 1; UNKNOWN_1.
PROSITE; PS00049; C2_DOMAIN 2; 1.
PROSITE; PS01159; WW_DOMAIN 1; 4.
                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity 88.9°
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                        PRELIMINARY;
                                    Query Match
Best Local Similarity
Thes 37; Conserva
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571 AA;
                  455 AA;
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"The distal convoluted tubule of rabbit kidney does not express a functional sodium channel.";
Am. J. Physiol. Renal Physiol. 280:F530-F539(2001).
EMBL, AF229024; AAF45194.1;
HSSP; Q62940; 115H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Ubiquitin-protein ligase Nedd4 (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21113801; PubMed=11181416;
Velazquez H., Silva T., Andujar E., Desir G.V., Ellison D.H.,
                                                                                                                                                                                                                                                                      PROSITE; PS00499; C2 DOMAIN 1; 1.
PROSITE; PS5004; C2 DOMAIN 2; 1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW DOMAIN 2; 4.
Ligase; Repeat; Ubl Conjugation; Ubl conjugation pathway.
DOMAIN 9 PRO-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967 967 Ubiquitin (By similarity).
1000 AA; 114936 MW; 3728088E50C149CB CRC64;
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C2 domain.
Poly-Gln.
WW 2.
WW 3.
HECT.
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InterPro; IPR008973; C2_CalB.
InterPro; IPR001202; WW_Rsp5_WWP.
                                                                    InterPro; IPR000008; C2.
InterPro; IPR008973; C2 Calb.
InterPro; IPR000569; HECT.
InterPro; IPR001202; WW_RSp5_WWP.
Pfam; PP00168; C2; 1.
Pfam; PP006128; HECT; 1.
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MARRY; SMO0456; WW; 4.

PROSITE; PS01159; WW DOWAIN 1; 4.

PROSITE; PS50020; WW DOMAIN 2; 4.
                                                                                                                                                                                               PRINTS; PR00360; C2DOMAIN.
SMART; SM00239; C2; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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1es 38; Conservative
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                    NEDD4.
                  Genew; HGNC:7727; NEDD4.H-InvDB; HX0012269; -.MIM; 602278;
 HSSP; Q62940; 115H.
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Q9N134;
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Nature 409:685-690(2001)
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                                           SEQUENCE FROM N.A.
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                          Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBIrel. 23, Last sequence update)
01-OCT-2003 (TrEMBIrel. 25, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
anriched 11brary, clone:A730011F13 product:neural cell expressed,
developmentally down-regulated gene 4b, full insert sequence.
Name=Nedd41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALM-C57BL/6J; TISSUE=Cerebellum;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    820 AA; 95282 MW; 0FDB34B29B3F4123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDDRLKFP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FLPKGWEVRHAPNGRPFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.6%; Score 187; DB 2;
88.9%; Pred. No. 2.5e-15;
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PROSITE; PS50237; WM DOMAIN 1; 3.
PROSITE; PS50020; WW DOMAIN 2; 3.
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002349; WW.
InterPro; IPR001202; WW_Rsp5_WWP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                               InterPro; IPR000008; C2.
InterPro; IPR008973; C2 Calb.
InterPro; IPR000569; HECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00403; WWDOMAIN.
SMART; SM00239; C2; 1.
SMART; SM00119; HECTC; 1.
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00456; WW; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 32; Conserv
                                                                                               SEQUENCE FROM N.A.
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                                                            NCBI_TaxID=9606;
                                                                                                                   ISSUE=Testis;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
STRAIN=CSTBL/6J; TISSUE=Cerebellum;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
manalysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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REMBL, AKO42621; BAC31307.1; -. BENDL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKE integrated sequence analysis (RISA) system-184-format Genome Res. 10:1757-1771(2000).
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004612; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR000569; HECT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.6%; Score 187; DB 2; 188.9%; Pred. No. 2.6e-15; ive 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Cerebellum;
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Pfam; PP00532; HECT; 1.
Pfam; PR00397; WW; 4.
PRINTS; PR00403; WWDOMAIN.
SMART; SM00119; HECTC; 1.
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SROSITE; PS01159; WW DOWAIN 1; 4.
PROSITE; PS50020; WW DOWAIN 2; 4.
SEQUENCE 835 AA; 96410 MW; 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Conservative
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us-09-385-918-5.rup

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Uterus;
                      SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099PK2;
01-JUN-2001 (
01-JUN-2001 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                          rissue-skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q99PK2
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                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE-21828840; PubMed=11840194; DOI=10.1038/sj.ejhg.5200747;
MEDILINE-21828840; Nebmed=11840194; DOI=10.1038/sj.ejhg.5200747;
Chen H., Ross C.A., Wang N., Huo Y., MacKinnon D.F., Potash J.B.,
Simpson S.G., McMahon F.J., DePaulo J.R., Jr., McInnis M.G.;
"NEDDAL on human chromosome 18421 has multiple forms of transcripts and is a homologue of the mouse Nedd4-2 gene.";
Eur. J. Hum. Genet. 9:922-930(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo Sapiens (Human).
Bukaryotaj Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-29804012; PubMed=14615060; DOI=10.1016/j.mce.2003.08.009;
Qi H., Grenier J., Fournier A., Labrie C.;
"Androgens differentially regulate the expression of NEDD4L
                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NEDD4La (Ubiquitin ligase NEDD4Lb) (Ubiquitin ligase NEDD4f)
Name=NEDD4La; Synonyms-NEDD4L;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 854;
                                                                                                                                                                                                                                                                                                                                 transcripts in LNCaP human proseate cancer cells.";
Mol. Cell. Endocrinol. 210:51-62(2003).
EMBL; AR210730; AAA45208.1; -
EMBL; AR38531; AAM46208.1; -
EMBL; AY112983; AAM46208.1; -
EMBL; AY112983; AAM46208.1; -
HSSP; Q62940; 115H.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0016874; F:lubiquitin-procein ligase activity; IEA.
GO; GO:0004842; F:ubiquitin cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      854 AA; 98180 MW; 00C74E1661F52E7F CRC64;
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Last annotation update)
protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 187; DB 2;
Pred. No. 2.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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SWART; SM00119; HECTC; 1.
SMART; SM00456; WW, 4.
PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000569; HECT.
InterPro; IPR002349; WW.
InterPro; IPR001202; WW.RepS_WWP.
Pfam; PP00632; HECT; 1.
Pfam; PP00397; WW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDD4L protein (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.6%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity soc...
32; Conservative
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE
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                                             Q9H2W4
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09BW58
1D 09BW
AC 09BW
DT 01-J
DT 01-J
DE NEDD
GN Name
OS Homo
OC EUKa
                     RESULT 6
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A REDELINE = 2238827; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F., Stachento L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Multing M., Touchman J.W., Green E.D., Dickson M.C., Rzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., T. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR00859; HECT.
InterPro; IPR00569; HECT.
InterPro; IPR001349; WW.
InterPro; IPR001202; WW.Rsp5_WWP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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88.9%; Pred. No. 2.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 AA.
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PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW DOMAIN 2; 4.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (DEC-2001) to the
EMBL; BC00621; AAH00621.2;
EMBL; BC019945; AAH19345.1;
HSSP; Q62940; 115H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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Pfam; PF00397; WW; 4.
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Nedd41 protein (Fragment).
Name=Nedd41;
Mus musculus (Mouse).
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Best Local Similarity 88.99
Matches 32, Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor. C3;

STRAIN=FVB/N; TISSUE=Kidney, and Mammary tumor. C3;

MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                      SEQUENCE FROM N.A.
STRALT-ESTBL/6 Norl BR;
MEDLINE=21067027: PubMed=11149908;
Kamynina E., Debonneville C., Bens M., Vandewalle A., Staub O.;
"A novel mouse Nedd4 protein suppresses the activity of the epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Neural cell expressed, developmentally down-regulated gene
                                                                                                                                                                                              EMBL, AF277232; AAK00809.1; -.
EMBL, AF277232; AAK00809.1; -.
EMBL, MGI:1933754; Nedd41.
GO; GO:0005622; Cintracellular; IEA.
GO; GO:0006842; Fiubiquitin-protein ligase activity; IEA.
GO; GO:0005512; Piubiquitin cycle; IEA.
InterPro; IPR002349; WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.6%; Score 187; DB 2; Length 85 ilarity 88.9%; Pred. No. 2.6e-15; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50237; HECT; 1.
PROSITE; PS01159; WW DOMAIN 1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR001202; WW_Rsp5_WWP.
Ubiquitin-protein ligase Nedd4-2
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SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00632; HECT; 1. Pfam; PF00397; WW; 4.
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                              Mus musculus (Mouse)
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                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                      Na+ channel."
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Best Local Simi]
Matches 32; (
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SEQUENCE
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Pahey J., Helton E., Ketteman M., Madan A., Rodrígues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krayulogac A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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PubMed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; BC03946; AAH39746.1; -

EMBL; BC071210; AAH71210.1; -.

HSSP; Q62940; ILSH.

MGD; MGI:1933754; Nedd41.

MGD; MGI:0005622; C:intracellular; IEA.

GO; GO:0006442; F:ubiquitin-protein ligase activity; IEA.

GO; GO:000652; P:ubiquitin-grotein ligase activity; IEA.

InterPro; IPR000569; HECT.
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS01159; WM DOWAIN 1; 4.
PROSITE; PS0020; WW DOWAIN 2; 4.
PROSITE; PS50020; WW DOWAIN 2; 4.
PROSITE; PS50020; WW DOWAIN 2; 5.
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88.9%; Pred. No. 2.6e-15;
iive 1; Mismatches 3;
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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Pfam; PF00632; HECT; 1.
Pfam; PF00397; WW; 4.
SMRINTS, PR00403; WWDOMAIN.
SWART; SM00119; HECTc; 1.
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STRAIN=FVB/N; TISSUE=Kidney;
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RESULT 12
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**Straubberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

**Straubberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

**Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

**Altschul S.P., Joedan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Batchenco M., Soares M.B., Bonaldo M.F., Casuvant T.L., Scheetz T.E.,

**Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

**Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**Villaton D.K., Muzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

**Restaley R.W., Touchman J.W., Grenn E.D., Dickson M.C.,

**Rahasley R.W., Touchman J.W., Grenn E.D., Dickson M.C.,

**Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Schnerch A., Schein J.E.,

**Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman B.J., Shevchenko Y., Bouffard G.G., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Kroyninski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                       84.6%; Score 187; DB 2; Length 875;
88.9%; Pred. No. 2.7e-15;
iive 1; Mismatches 3; Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL, BC022897; AAH32597.1; -.
                                                                                                                                                                                                                                              Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases EMBL; BC082281; AAH82281.1; -
                                                                                                                                                                                                                                                                                       SEQUENCE 875 AA; 101627 MW; 7662C1958052FC3E CRC64;
                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                       and mouse cDNA sequences.";
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Best Local Similarity 88.50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                TISSUE=Eye;
Director MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22980412; PubMed=14615060; DOI=10.1016/j.mce.2003.08.009;
Qi H., Granier J., Fournier A., Labrie C.;
"Androgens differentially regulate the expression of NEDD4L transcripts in LNCaP human prostate cancer cells.";
MOI Cell. Endocrinol. 210:51-62(2003).
-!- SIMILARITY: Contains 1 c. domain.
EMBL, AX112985; AAM76730.1; -.
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R GO; GO:0005624; F:ligase activity; IEA.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0006812; F:ubiquitin-protein ligase activity; IEA.

R GO; GO:0006512; F:ubiquitin cycle; IEA.

R InterPro; IPR00008; C2.

R InterPro; IPR00008; C2.

R InterPro; IPR000569; HECT.

R Ffam; PF00168; C2; 1.

R Ffam; PF00168; C2; 1.

R SMART; SM00119; HECT; 1.

R SMART; SM00119; HECT; 1.

R SMART; SM00119; HECT; 1.

R R SMART; SM00149; C2:DOMAIN_1; UNKNOWN_1.

R PROSITE; PS500049; C2:DOMAIN_2; 1.
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0006812; P:ubiquitin cycle; IEA.
InterPro; IPR00809; C2.
InterPro; IPR008973; C2 CalB.
InterPro; IPR008059; HECT.
InterPro; IPR002349; WW.
InterPro; IPR0012024; WW.RSP5_WWP.
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Last annotation update)
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88.9%; Pred. No. 2.8e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                      PRINTS; PRO0360; C2DONAIN.
PRINTS; PR00403; WWDOMAIN.
SMART; SM00139; C2; 1.
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 3.
PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
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                                                                                                                                                                                                               Pfam; PF00168; C2; 1. Pfam; PF00632; HECT; 1. Pfam; PF00397; WW; 3.
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Best Local Similarity
Matches 32; Conserv
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Ligase.
SEQUENCE
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Q7Z5F2
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MEDLINE20501262; PubMed=11046148;
MEDLINE20501262; PubMed=11046148;
MODI=10.1128/MCB.20.22.8526-8535.2000;
Winberg G., Matskova L., Chen F., Plant P., Rotin D., Gish G.,
Ingham R., Ernberg I., Pawson T.;
"Latent membrane protein 2A of Epstein-Barr virus binds WW domain E3
protein-ubiquitin ligases that ubiquitinate B-cell tyrosine kinases.";
Mol. Cell. Biol. 20:8526-8515(2000).
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOSI_TaxID=9606;
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"The Nedd4-like protein KTAA0439 is a potential regulator of the epithelial sodium channel.";
U. Biol. Chem. 276:8597-8601(2001).
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MEDLINE=21269431; PubMed=11244092; DOI=10.1074/jbc.C000906200;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 C2 domain.
EMBL; ABOTALIT9; BAB69424.1; -.
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GO; GO:0005622; F:protein binding; IPI.

GO; GO:0017080; F:protein binding; IPI.

GO; GO:0017080; F:protein binding; IPI.

GO; GO:0007588; P:excretion; NAS.

GO; GO:0004580; P:protein ubiquitination; NAS.

GO; GO:0004580; P:protein ubiquitination; NAS.

GO; GO:0016567; P:protein ubiquitination; NAS.

GO; GO:0016567; P:protein ubiquitination; NAS.

GO; GO:0010889; P:response to metal ion; IDA.

GO; GO:0010889; P:response to metal ion; IDA.

GO; GO:001040; P:response to metal ion; IDA.

GO; GO:001040; P:response to metal ion; IDA.

GO; GO:001040; P:response to metal ion; IDA.

R O: GO:001040; P:response to metal ion; IDA.

GO; GO:001040; P:response to metal ion; IDA.

R O: GO:001040; P:response to metal ion; IDA.

R O: GO:001040; P:response to metal ion; IDA.

R InterPro; IPR00059; MW.

R InterPro; IPR001202; WW.

R Pfam; PF00652; HGT.; I.

R Pfam; PF00652; HGT.; I.
                                                                                                                                                                     Length 947;
                                                                                                                                                                                                                                       3; Indels
                                                                                                  947 AA; 109429 MW; 95CB0FDEDCB96639 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NEDD4-like ubiquitin ligase 3.
                                                                                                                                                                                                                                                                                                                                             470 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 505
                                                                                                                                                                                                                                                                                                      2 FLPKGWEVRHAPNGRPFFIDHNTKTTTWEDPRLKIP 37
                                                                                                                                                                 84.6%; Score 187; DB 2;
88.9%; Pred. No. 2.9e-15;
live 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  955 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
PROSITE; PS01159; WW DOMAIN 1; 4. PROSITE; PS50020; WW DOMAIN 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00403; WWDOMAIN.
SMART; SM00239; C2; 1.
                                                                                                                                                                                                    Best Local Similarity 88.9
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=NEDL3;
                                                                      Ligase.
SEQUENCE
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96PUS
Q96PUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13

1096 PUS

10 966 PUS

10 966 PUS

10 966 PUS

11 966 PUS

11 966 PUS

12 966 PUS

13 966 PUS

14 96 PUS

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Ad H., Grenier J., Fournier A., Labrie C.;

Androgens differentially regulate the expression of NEDD4L

Transcripts in LNCaP human prostate cancer cells.";

MOI. Cell. Endocrinol. 210:51-62(2003).

EMEL; AX112984; AAM76729.1; -..

EMEL; AX112984; AAM76729.1; -..

EMEL; AX112984; AAM76729.1; -..

ROJ GO:0006822; C:intracellular; IEA.

GO; GO:0006842; F:ligase activity; IEA.

GO; GO:0006842; F:ubbquitin-protein ligase activity; IEA.

GO; GO:006842; F:ubbquitin-protein ligase activity; IEA.

GO; GO:0006812; P:ubbquitin-protein ligase activity; IEA.

ROJ GO:0006812; P:ubbquitin-protein ligase activity; IEA.

GO; GO:0006812; P:ubbquitin-protein ligase activity; IEA.

GO; GO:0006812; P:ubbquitin-protein ligase activity; IEA.

ROJ GO:0006812; P:ubbquitin-protein ligase activity; IEA.

GO; GO:0006812; P:ubbquitin-protein ligase activity; IEA.

GO:00006812; P:ubquitin-protein ligase activity; IEA.

GO:000006812; P:ubquitin-p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 3e-15;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Score 187; DB 2; Length 955;
Pred. No. 3e-15;
1; Mismatches 3; Indels
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SEQUENCE 967 AA; 111339 MW; 86940A75880539F7 CRC64;
                                                                                                                                                                                                                                                                                                                                    955 AA; 110021 MW; A8BB278A37F6A6B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ubiquitin ligase NEDD49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 513
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                                                                         PROSITE; PS00499; C2_DOMAIN_1; UNKNOWN_1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
PROSITE; PS50207; HECT; 1.
PROSITE; PS01159; WW_DOMAIN_1; 4.
PROSITE; PS50020; WW_DOMAIN_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 32; Conservative 1
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88.9%;
SMART; SM00119; HECTC; 1.
SMART; SM00456; WW; 4.
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es 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus lavis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 187; DB 2; Length 971;
88.9%; Pred. No. 3e-15;
tive 1; Mismatches 3; Indels
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PROSITE; PS50004; C2 DOMAIN_2; 1.
PROSITE; PS50237; HECT; 1.
PROSITE; PS50020; WW DOMAIN 1; 4.
PROSITE; PS50020; WW DOMAIN 2; 4.
SEQUENCE 971 AA; I11959 WW; F25536DC71612E03 CRC64;
                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nedd4 protein.
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                                                                                                     971 AA
                                                                                                     PRT;
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Best Local Similarity 88.9%
                                                                                                PRELIMINARY;
                                                                                                     042573
RESULT 15
042573
AC 042573
DT 01-JAM
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494 FLPPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFP 529

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Search completed: October 13, 2005, 15:09:23 Job time : 76.381 secs

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; Search time 13.5165 Seconds (without alignments) 171.684 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                          October 13, 2005, 14:01:04;
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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30
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                                                                                                                                                                                                   Perfect score:
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seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing:

Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

2105692

Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1980s: \*
geneseqp2000s: \*
geneseqp2000s: \*
geneseqp2001s: \*
geneseqp2001s: \*
geneseqp2003bs: \*
geneseqp2003bs: \* A\_Geneseq\_16Dec04:\* 4.0.07.8 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		inh	Sma	inh	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	ΡY	191	191	191	191
	uo	Viral	Human	Viral	Human	WBP-1	Human	Human	Human	Human																
	Description	Ada50768	Aab83031	Ada50788	Adk84421	Adk88045	Adk88545	Adk88044	Adk84919	Adk84968			Adk86562	Adk87588	Adk83902	Adk88578	Adk88349	Adk85989	Adk86505	Adk85516	Adk87020	Aar98323	Adk83656	Adk84646	Adk86759	Adk86754
SUMMALES		8		8	п	rs.	5	4	o	8	4	0	7	80	7	8	O	თ	5	9	0	9	9	9	o.	4
Maios	ID	ADA5076	AAB8303	ADA50788	ADK8442	ADK8804	ADK8854	ADK88044	ADK84919	ADK84968	ADK88384	ADK84460	ADK86562	ADK87588	ADK83902	ADK88578	ADK88349	ADK85989	ADK86505	ADK85516	ADK87020	AAR98323	ADK83656	ADK84646	ADK8675	ADK8675
	DB	9	4	9	æ	œ	80	æ	œ	œ	œ	80	8	œ	æ	œ	8	æ	œ	œ	æ	7	œ	ω	œ	8
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de	Query	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3
	Score	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
	Result No.	7	8	m	4	.Ω	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	191	E C	ayla	mot.	inyla	
Human	PPPPY	Biotinyla	PPPPY	Biotin																
Adk85170	Adk85755	Adk89547	Adk83605	Adk86224	Adk88674	Adk85778	Adk84124	Adk86828	Adk89444	Adk89120	Adk89613	Adk89614	Adk84704	Adk89376	Adk83562	Aaw38128	Adb49367	Aaw38123	Adb49362	
ADK85170	ADK85755	ADK89547	ADK83605	ADK86224	ADK88674	ADK85778	ADK84124	ADK86828	ADK89444	ADK89120	ADK89613	ADK89614	ADK84704	ADK89376	ADK83562	AAW38128	ADB49367	AAW38123	ADB49362	
8	æ	ω	œ	ω	œ	ω	ω	ω	ω	ω	œ	8	ω	œ	œ	7	7	7	7	
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	12	12	13	13	
93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	
28	28	28										28				28		28		
26	27	28	59	30		32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

PPXY motif; type I WW-domain; Nedd4; virucide; viral budding; virus propagation; viral infection; hepatitis B virus; human herpes virus 1. Viral inhibitor peptide SEQ ID NO:5. ADA50768 standard; peptide; 5 AA. 20-NOV-2003 (first entry) WO2003015714-A2. Unidentified 27-FEB-2003 ADA50768; ADA50768 

21-AUG-2002; 2002WO-US026681

21-AUG-2001; 2001US-0313883P (MYRI-) MYRIAD GENETICS INC.

Hobden A; Zavitz K, WPI; 2003-300559/29. Morham S,

Disclosure; Page 12; 75pp; English.

Novel peptide capable of binding to type I WW-domain of Nedd4 protein and useful for treating viral infections, comprises contiguous amino acid sequence of a viral protein encompassing PPXY motif.

The invention relates to a novel isolated peptide comprising a contiguous amino acid sequence of 8-30 amino acid residues of a viral protein, where the contiguous amino acid sequence encompasses the PPXY motif of the viral protein and the peptide is capable of binding at type I WW-domain of the Nedd4 protein. A peptide of the invention has virucide activity, and arcs as an inhibitor of viral budding and virus propagation. The peptides are useful in the manufacture of a medicament useful in the treatment of viral infections caused by a virus selected from hepatitis B virus and human hepps virus 1. The peptides are also useful for inhibiting viral budding from virus infected cells and thus inhibiting virus propagation in the cells. The present sequence represents a peptide of the invention.

N

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Indels

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Mismatches

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Conservative

4

Matches

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The present sequence is the Smad PY motif consensus sequence. The PY motif binds to the WW domain of HBCT (homologous to B6 carboxyl terminus) E3 ubiquitin ligase. resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated bignalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase W domain to Smad PY motif, on the callular ubiquitination of Smad protein by E3 ubiquitin ligase, or on the callular cavels of Smad protein hECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BWP-mediated cell cignalling. Agents that inhibit BWP-mediated signalling are useful for signalling are useful for stimulating bone that unwament BWP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating energy, inflammation, neurodegeneration and fibrosis
                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                                                                                                                                                                                                                                                                          Human, HECT; homologous to E6 carboxyl terminus; ubiquitination, HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif; Smad 1; Smad 5.
                                                                               Gaps
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                                        Length 5;
                                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                      Human Smad 1 and Smad 5 PY motif consensus sequence.
                                  Score 28; DB 6; L
Pred. No. 1.8e+06;
0; Mismatches 1;
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                                                                                                                                                                                                                                                        AAB83031 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 35; 75pp; English.
                                        93.3%;
80.0%;
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                                                                             Conservative
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                Query Match
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                                                                                                                   2 PPPXY 6
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  Sequence 5 AA;
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide capable of binding to type I WW-domain of Nedd4 protein and useful for treating viral infections, comprises contiguous amino acid sequence of a viral protein encompassing PPXX motif.
Gaps
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                                                                                                                                                                                                                                                         PPXY motif; type I WW-domain; Nedd4; virucide; viral budding; virus propagation; viral infection; hepatitis B virus; human herpes virus 1.
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                                                                                                                                                                                                                                     Viral inhibitor peptide SEQ ID NO:25
                                                                                                                                         ADA50788 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-2002; 2002WO-US026681.
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The present invention relates to novel compositions comprising peptides (ADK83300-ADK89584) from 191P4012(b) and related proteins. It was found that 191P4012(b), which maps to chromosome 1422-423.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humonral or cellular immune response. To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
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                                                                                                                                                                                                                                                                                                                New composition comprising 191P4D12(b) proteins and polynucleotides, useful in diagnosing, preventing and treating cancer, e.g. prostate, bladder, kidney, colon, lung, pancreas or ovary and in eliciting a humoral or cellular immune response.
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80.0%; Pred. No. 1.8e+06;
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01-NOV-2002; 2002US-0423290P.
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WO2004016799-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; Immunostimulant; Vaccine; Gene Therapy, 191P4D12(b); cancer; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; pancer; cancer; pancer; or cancer; breast cancer; uterus cancer; cervix cancer; immune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
                                                   Cytostatic; Immunostimulant; Vaccine; Gene Therapy, 191P4D12(b); cancer; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; pancer; oancer; oancer; oancer; oancer; oancer; oancer; oancer; oancer; umune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to novel compositions comprising peptides
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               Human 191P4D12(b) peptide fragment #1122.
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01-NOV-2002; 2002US-0423290P.
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80.0%;
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                                                                                                                                                   The present invention relates to novel compositions comprising peptides (ADK83300-ADK90584) from 191P4D12(b) and related proteins. It was found that 191P4D12(b), which maps to chromosome 1q22-q23.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humoral or cellular immune response. To isolate genes that are overxpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; brung cancer; pancer; oancer; pancer; oancer; cervix cancer; immune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
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                                                                    useful in diagnosing, preventing and treating cancer, e.g. prostate, bladder, kidney, colon, lung, pancreas or ovary and in eliciting a humoral or cellular immune response.
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                                                       composition comprising 191P4D12(b) proteins and polynucleotides
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                                                                                                                                                                                                                                                                                  derived from prostate cancer tissues.
                                                                                                                         Claim 1; Page 205; 443pp; English.
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 Challita-Eid PM,
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01-NOV-2002; 2002US-0423290P.
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                           WPI; 2004-203808/19
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Best Local Similarity
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 Raitano AB,
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Claim 1; Page 199; 443pp; English

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The present invention relates to novel compositions comprising peptides (ADK83300-ADK90584) from 191P4012(b) and related proteins. It was found that 191P4012(b), which maps to chromosome 1422-423.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humoral or cellular immune response. To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
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Pred. No. 1.8e+06;
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                                                                                                                                                                                               derived from prostate cancer tissues.
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01-NOV-2002; 2002US-0423290P.
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The present invention relates to novel compositions comprising peptides (ADK83300-ADK99584) from 191P4D12(b) and related proteins. It was found that 191P4D12(b), which maps to chromosome 1922-923.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humoral or cellular immune response. To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA
                                                                                                                                                                                                Cytostatic; Immunostimulant; Vaccine; Gene Therapy; 191P4D12(b); cancer; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; parcers cancer; oancer; parcer; cancer; uterus cancer; cancer; immune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
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Pred. No. 1.8e+06;
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                                                                                                                                                                Human 191P4D12(b) peptide fragment #5085.
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                                          ADK88384 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                          Human 191P4D12(b) peptide fragment #1669.
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                                    93.3%;
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Sequence 9 AA;
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The present invention relates to novel compositions comprising peptides (ADK83300-ADK90584) from 191P4012(b) and related proteins. It was found that 191P4012(b), which maps to chromosome 1922-431.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in aliciting a humoral or cellular immune response. To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA derived from prostate cancer tissues.
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                                                                                                                                                                                                                                              New composition comprising 191P4D12(b) proteins and polynucleotides, useful in diagnosing, preventing and treating cancer, e.g. prostate, bladder, kidney, colon, lung, pancreas or ovary and in eliciting a humoral or cellular immune response.
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Pred. No. 1.8e+06;
0; Mismatches 1; Indels
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                     lung cancer; pancreas cancer; ovary cancer; breast cancer; uterus cancer; cervix cancer; immune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in diagnosing, preventing and treating cancer, e.g. prostate, bladder, kidney, colon, lung, pancreas or ovary and in eliciting a humoral or cellular immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising 191P4D12(b) proteins and polynucleotides,
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prostate cancer; bladder cancer; kidney cancer; colon cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 155; 443pp; English.
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01-NOV-2002; 2002US-0423290P.
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Faris M,

Jakobovits A,

Challita-Eid PM,

Raitano AB,

WO2004016799-A2

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26-FEB-2004

20-MAY-2004

ADK86562;

Query Match

Matches

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WPI; 2004-203808/19

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                                                                                                                           The present invention relates to novel compositions comprising peptides tho ADMS036491 from 191P4D12 (b) and related proteins. It was found that 191P4D12 (b), which maps to chromosome 1q22-q23.2, is aberrantly expressed in a number of cancers and so the compositions of the invention are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humoral or cellular immune response. To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridiaation (SSH) method was used, using cDNA derived from prostate cancer tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; Immunostimulant; Vaccine; Gene Therapy, 191P4D12(b); cancer; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; pancer; oancer; oancer; oancer; oancer; oancer; cervix cancer; immune response; human; chromosome 1q22-q23.2; Suppression Subtractive Hybridisation; SSH.
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New composition comprising 191P4D12(b) proteins and polynuclectides, useful in diagnosing, preventing and treating cancer, e.g. prostate, bladder, kidney, colon, lung, pancreas or ovary and in eliciting a humoral or cellular immune response.
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                                                                                           Claim 1; Page 193; 443pp; English
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01-NOV-2002; 2002US-0423290P.
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are useful in diagnosing, preventing and treating cancer, e.g. cancer of the prostate, bladder, kidney, colon, lung, pancreas, ovary, breast, uterus or cervix and in eliciting a humoral or cellular immune response.
                                                  To isolate genes that are overexpressed in prostate cancer, the Suppression Subtractive Hybridisation (SSH) method was used, using cDNA derived from prostate cancer tissues.
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                                                                                                                                                          Length 9;
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Pred. No. 1.8e+06;
0; Mismatches 1;
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Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                     ADK88578 standard; peptide; 9 AA.
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ADK88578
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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 2 pppxx 6

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Search completed: October 13, 2005, 15:00:34
Job time: 15:5165 secs

1103, Ap 27933, A 40283, A 55499, A 10130, A

Sequence

Sequence 55499, A Sequence 10130, A Sequence 13180, A Sequence 29054, A Sequence 2624, Appl Sequence 44, Appl Sequence 27, Appl Sequence 74, Appl Sequence 74, Appl Sequence 16847, A Sequence 16847, A Sequence 16847, A Sequence 401, Appl Sequence 102, Appl Sequ

Scoring table:

Minimum DB Maximum DB

Database

Result

score:

Title: Perfect

Sequence:

OM protein

Run on:

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APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
TITLE OF INVENTION: SIGNALLING DOMAIN THEREIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: THEREOF
INVENTION: THEREOF
INVENTION: THEREOF
INVANIES OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
ZIP: 07601
US-09-640-211A-1103
US-09-248-796A-27933
US-09-270-767-55499
US-09-270-767-55499
US-09-902-540-10130
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US-09-270-76-59054
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US-09-270-76-52037
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US-09-240-211A-2262
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US-09-240-108-063-27
US-09-241-155-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-DEC-1994
CLASSIFICATION:
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NAME: Jackson Esq., David A.
REGISTRAILON NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEFAN: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 35:
SEGUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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80.0%; Pred. No. 50;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/08476509B; Patent No. 6034212; GENERAL INFORMATION:
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HYPOTHETICAL: NO
US-08-476-509B-35
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STRANDEDNESS: si
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Best Local Similarity
Matches 4; Conserv
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6022, Ap
33978, A
49195, A
58296, A
6393, Ap
25578, A
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50500, A
6691, Ap
22, Appl
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                                                                                                                       ; Search time 2.85714 Seconds (without alignments) 156.763 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Compugen Ltd
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US-08-630-916A-54
US-08-644-312-12
US-08-844-312-12
US-08-844-312-15
US-08-844-312-16
US-08-844-312-16
US-09-444-791A-19
US-09-444-791A-19
US-09-444-791A-19
US-09-444-791A-19
US-09-38-55
US-09-38-55
US-09-314-268-156
US-09-270-767-50500
US-09-213-999-6691
US-09-213-999-6691
US-09-213-976-6022
US-09-213-976-6022
US-09-270-767-5925
US-09-270-767-5825
US-09-270-767-5825
US-09-270-767-5825
US-09-218-976-6022
US-09-270-76-6022
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US-09-270-76-5825
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-08-469-260A-48
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US-08-467-344A-48
US-08-424-550B-48
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                    GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       protein search, using sw model
                                                                                                                           October 13, 2005, 13:50:53
                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                         US-09-385-918-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyright
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Gaps

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Length 10;

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RESULT 4
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                                                                                                           US-08-630-916A-54

Sequence 54, Application US/08630916A

Sequence 54, Application US/08630916A

Patent No. 6011137

Patent No. 6011137

APPLICANT: Pirozzi, Gregorio

APPLICANT: Powlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds

SIRRET: New York

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-844-312-12
US-08-844-312-12
US-08-844-312-12
Sequence 12, Application US/08844312
Fatent No. 5948639
GENERAL INFORMATION:
APPLICANT: Carlos J. Gimeno and Dean A. Falb
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 66;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.v
Fra 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109-1875
PPPXY 6
                              3 PPPAY 7
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Sequence 15, Application US/08844312;
Sequence 15, Application US/08844312;
Patent No. 5948639;
Patent No. 5948639;
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 2
Pred. No. 74;
0; Mismatches
                                                                                                                          PPDLICALION:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT: INFORMATION:
NAME: 39,030
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-013
TELECOMMUNICATION INFORMATION:
TELECHOUS: (617)227-7400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTER.STICS:
LENGTH: 16 amino acids
"WITE: amino acids
"WITE: ABOUTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MULECULE TYPE: peptide
US-08-844-312-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 60 State Stre
CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PPPXY 6
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APPLICANT: Chambers, James
APPLICANT: Causey, Stuart
APPLICANT: Causey, Stuart
APPLICANT: Pollock, Thomas J.
APPLICANT: Cappello, Joseph
APPLICANT: Crissman, John W.
TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same CORRESPONDENCE ADDRESS:
      Dorman, Mary A
/ENTION: No. 5770697el Peptides Comprising Repetitive
/ENTION: Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
      TITLE OF INVENTION: No. 5770697el Peptides Comprising I TITLE OF INVENTION: No. 5770697el Peptides Comprising I TITLE OF INVENTION: Units of Amino Acids and DNA Sequer NUMBER OF SEQUENCES: 112
CORRESPONDENCE ADDRESS: ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco STATE: California
CONNTRY: US
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURSET APPLICATION DATA:
APPLICATION NUMBER: US 08/477,509B
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OCT-1987
PRIOR APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTOONRY/AGENT INFORMATION:
ANAME: DECAPT INFORMATION:
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-7/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 6018030
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Richardson, Charles
APPLICANT: Chambers, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-20 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-477-509B-19
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US-08-482-085B-19
   APPLICANT:
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Patent No. 5948639
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway Genes NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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                                                                                                                                             DB 2; Length 16; 74;
                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPRY disk
COMPUTER: PROPRY AND FOLDOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
FILING DATE:
                                                                                                                                                Score 28; DB 2
Pred. No. 74;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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US-08-477-509B-19
Sequence 19, Application US/08477509B
Sequence 19, Application US/08477509B
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Cappello, John w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNI-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                             93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
COUNTRY: USA
; TYPE: amino acid
; TOPOLOGY: linear
WOLECULE TYPE: peptide
US-08-844-312-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-844-312-16
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Gaps
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APPLICANT: DEVARE, SURFIL G
APPLICANT: DESAL, SURESH M
APPLICANT: CASET, JAMES M
APPLICANT: CASET, JAMES M
APPLICANT: CASET, JAMES M
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: STEWART, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: 
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                          COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEADS MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/444,791A
FILING DATE: 22-No. 6355776-1999
CLASSIFICATION: VUNROWN>
PRIOR APPLICATION: VUNROWN>
PRIOR APPLICATION NUMBER: US 08/482,085
FILING DATE: 07-40N-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-APR-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-APR-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-APR-1993
APPLICATION NUMBER: US 06/927,258
FILING DATE: OF-ANOV-1986
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 3;
Pred. No. 78;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/08867611
Patent No. 6172189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%;
80.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 PPPTY 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
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Patent No. 6335776
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.3%; Score 28; DB 3; Length 17; 80.0%; Pred. No. 78;
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3: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                               COMPUTER FRANKELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/482,085B
FILING DATE: 04-NOV-1986
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OCT-1987
RIOR APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
RRIOR APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: TECARTION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
       ADDRESSEE: Flehr, Hobbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
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                          STREET: Four CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPPTY 15
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US-09-444-791A-19
                                                                                                                                              COUNTRY:
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Sequence 156 Application US/09314268

Patent No. 6346377

GENERAL INFORMATION:

APPLICANT: DOORDAY.

TITLE OF INVENTION: INFOVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIRUSES

FILE REFERENCE: 3789/80902

CURRENT APPLICATION NUMBER: US/09/314,268

EARLIER FILING DATE: 1999-03-19

EARLIER FILING DATE: 1999-05-18

EARLIER FILING DATE: 1999-05-18

SEALIER FILING DATE: 1999-05-18

SOFTWARE: PATENTIN UND: 179

SEQ ID NOS: 179

SEQ ID NO 156

FAMORY
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                                                                                                        COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/690,359
FILING DATE: 17-OCC-2000
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATE:

APPLICATION NUMBER: 08/867,611

FILING DATE: 02-JUN-1997

APPLICATION NUMBER: US/08/646,757

FILING DATE: cURKNOWN>

APPLICATION NUMBER: US/08/179,896

FILING DATE: 4DKROWN>

APPLICATION NUMBER: US 07/572,822

FILING DATE: 24-AUG-1990

APPLICATION NUMBER: US 07/748,561

FILING DATE: 21-AUG-1991

APPLICATION NUMBER: US 07/748,565

FILING DATE: 21-AUG-1991

APPLICATION NUMBER: US 07/748,565

FILING DATE: 21-AUG-1991

APPLICATION NUMBER: US 07/748,565

FILING DATE: 21-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-690-359-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: POREMBSKI, PRISCILLA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
                                              ZIP: 60064-3500
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STEWART, JAMES L
RUPBECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-MUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E
                                                                                                        FILING DATE: 02-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
APPLICATION NUMBER: US/08/179,896
FILING DATE:
                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: POREMBSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REPERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
FILING DATE: 02-UUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVARE, SUSHIL G
DESAI, SURESH M
CASEY, JAMES M
DALLEY, STEPHEN H
DAWSON, GEORGE J
GUTIERREZ, ROBIN A
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-690-359-55
; Sequence 55, Application US/09690359
; Patent No. 6593083
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTIGENS
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0.
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708-937-9556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DEVARE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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            ; OTHER INFORMATION: Description of Unknown Organism: No. 6346377-Human Virus
US-09-314-268-156
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                                                                                                                                                                                                                                                                  Sequence 35283, Application US/09270767

Faceria No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburgar et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 35283

LENGTH: 52
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Sequence 50500, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 50500

LENGTH: 52
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.3%; Score 28; DB 4; Length 52;
80.0%; Pred. No. 2e+02;
.ive 0; Mismatches 1; Indels
                                                                                   93.3%; Score 28; DB 3; Length 39;
80.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 1; Indels
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US-09-513-999C-6691
Sequence 6691, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-35283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50500
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80.0%;
                                                                 Query Match
Best Local Similarity 80.0-
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Best Local Similarity
                                                                                                                                                                                         10 PPPAY 14
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ORGANISM: Unknown
                                                                                                                                                                                                                                              RESULT 12
US-09-270-767-35283
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US-09-270-767-50500
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APPLICANT: Duclert.
APPLICANT: Duclert.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
Patent No. 6783961
CURRENT FILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
SOFTWARE: Patent.pm
SEQ ID NO 6691
LENGTH: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-09-154-083-22
; Sequence 22, Application US/09154083
; Sequence 22, Application US/09154083
; GENERAL INFORMATION:
; APPLICANT: Wu, Kai
; TITLE OF INVENTION: Constructs Therefor
; FILE REPERENCE: 30062-20022.00 Polyketide Synthase Enz
; CURRENT APPLICATION NUMBER: US/09/154,083
; CURRENT PILION DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.3%; Score 28; DB 3; Length 63; 80.0%; Pred. No. 2.46+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 13, 2005, 14:03:06 Job time : 3.98214 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 22

: LENGTH: 63

: TYPE: PRT

; ORGANISM: Streptomyces hygroscopicus

US-09-154-083-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.0.
امار 4; Conservative
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 PPPAY 54
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us-09-385-918-15.rapb

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4; Conservative
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Best Local Similarity
Matches 4; Conser
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US-10-307-956-16
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Sequence 16, Appl
Sequence 25, Appl
Sequence 173, Appl
Sequence 27, Appl
Sequence 24, Appl
Sequence 140, Appl
Sequence 17, Appl
Sequence 27, Appl
Sequence 23, Appl
                                                                                                             October 13, 2005, 13:59:34; Search time 12.7912 Seconds (without alignments) 195.471 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

(cgn2_6/ptodata/1/pubpaa/DSO7_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/DSO7_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/DSO6_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

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(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-307-956-16
US-10-226-007-25
US-10-185-050-178
US-10-185-050-168
US-10-185-050-140
US-10-185-050-140
US-10-185-050-140
US-10-307-956-12
US-10-307-956-22
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                                                                                                                                                                                                                                                                                                                         1859788 segs, 416717961 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                  seg length: 0
seg length: 200000000
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                                                                                                                                                                                                                             1 XPPPXY 6
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Match
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                                                                                                                                                                                                              Perfect score:
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No.
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sequence 5, Application US/10226007

publication No. US20030105277A1

GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Abrian

TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

TITLE OF INVENTION UNMBER: US/10/226,007

CURRENT APPLICATION NUMBER: US 60/313,883

PRIOR APPLICATION NUMBER: US 60/313,883

PRIOR FILING DATE: 2001-08-21

NUMBER OF SEQ ID NOS: 1673

SEQ ID NO 5

LENGTH: 5

LENGTH: 5
 Sequence 225, App Sequence 170, App Sequence 170, App Sequence 171, App Sequence 171, App Sequence 111, App Sequence 216, App Sequence 224011, App Sequence 224011, App Sequence 226064, Sequence 27771, A Sequence 218513, Sequence 2118513, Sequence 221354, Sequence 221354, Sequence 221354, Sequence 221354, Sequence 222092, Sequence 222092, Sequence 25502, Sequence 25602, Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6192, Ap
9, Appli
268179,
168512,
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Sequence
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US-10-185-050-229
US-10-185-050-229
US-10-185-050-170
US-10-185-050-170
US-10-185-050-171
US-10-086-2195-191
US-10-086-195-911
US-10-086-2195-916
US-10-086-195-911
US-10-086-2195-911
US-10-424-599-224011
US-10-424-599-224011
US-10-425-115-286555
US-10-425-115-286555
US-10-425-115-316082
US-10-425-115-316082
US-10-424-599-258502
US-10-424-599-175735
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80.0%; Pred. No. 1.7e+06;
iive 0; Mismatches 1;
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                                      , ORGANISM: Homo sapiens
US-10-226-007-5
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Gaps

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ABLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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80.0%; Pred. No. 4.38+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 28-Jun-2002
CLASSIFICATION: <UNANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE: 03-Apr-1997
ATTORNEY/AGEM'INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 896-8090
TELEFAX: (212) 896-8090
TELEFX: (212) 896-8090
TELEX: (611) PONIE
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                         the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 173:
US-10-185-050-173
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 168, Application US/10185050; Publication No. US20030077577A1
GENERAL INFORMATION:
                                                                                                                                                             ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: <Unknown>
                                                                    STREET: 1155 Avenue of CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 12 amino acids
  NUMBER OF SEQUENCES: 233
                                                                                           CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25, Application US/10226007

Sequence 25, Application No. US20030105277A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Morham, Scott

APPLICANT: Zavitz, Kenton

TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

CURRENT APPLICATION NUMBER: US/10/226,007

CURRENT APPLICATION NUMBER: US 60/313,883

PRIOR APPLICATION NUMBER: US 60/313,883

PRIOR PILING DATE: 2001-08-21

NUMBER OF SEQ ID NOS: 1673

SOFTWARE: Patentin version 3.1
                                                            APPLICANT: Hoekstra, Merl F.
APPLICANT: Xie, Weilin
APPLICANT: Xie, Weilin
APPLICANT: Micray, Erank
APPLICANT: Micray, Erank
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 866098 433
CURRENT APPLICATION NUMBER: US/10/307,956
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US/9/385,918
PRIOR APPLICATION NUMBER: US/9/385,918
PRIOR FILING DATE: 1999-08-30
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 6
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; Publication No. US20030077577A1
; GENERAL INFORMATION:
Sequence 16, Application US/10307956 Publication No. US20030119072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien
US-10-307-956-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 140, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Gregorio
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFFCATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.3%; Score 28; DB 14; Length 14; 80.0%; Pred. No. 4.9e+02; Live 0; Mismatches 1; Indels
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                    NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRAX: (212) 896-8864/9741
                                                                                                                                                                                      CURRENT APPLICATION DATA:

RAPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Unn-2002
CLASSIFICATION - Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                 COUNTRY: USA
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Best Local Similarity
Matches 4; Conserva
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US-10-185-050-140
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Publication No. US200007757741
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: DOLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hildebrandt, Friedhelm
APPLICANT: Jentsch, Thomas J.
TITLE OF INVENTION: BSND Nucleic Acids and Proteins
FILE REFERENCE: UM-07447
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEFAX: (212) 896-8864/9741
TELEX: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 14;
Pred. No. 4.6e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 15;
Pred. No. 4.6e+02;
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ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 168:
US-10-185-050-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/273,476
CURRENT FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Petentin version 3.2
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-273-476-27
; Sequence 27, Application US/10273476
; Publication No. US20040023234A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%; Scur
80.0%; Pred
0;
                                                                                                                                                                                                                                                                                                          LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
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Best Local Similarity 80.v
Loc 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-273-476-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserva
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US-10-185-050-54
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Sequence 225, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
    APPLICANT: Pirozzi, Gregorio
    APPLICANT: Pirozzi, Gregorio
    Fowlkes, Dana M.
    TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
    POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REPREMENTE: 860098.433
CURRENT APPLICATION NUMBER: US/10/307,956
PRIOR APPLICATION NUMBER: US/09/385,918
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FRASEREQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Application US/10307956
Publication No. US2003011907241
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
APPLICANT: Xie, Weilin
APPLICANT: Xie, Weilin
TILE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 860098.433
CURRENT APPLICATION NUMBER: US/10/307,956
CURRENT FILING DATE: 2002.12-02
PRIOR APPLICATION NUMBER: US/09/385,918
PRIOR PLILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 4.9e+02;
0; Mismatches 1; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREFT: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.3%;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO 23
; LENGTH: 14
; TYPE: PRT
ORGANISM: Homo sapien
US-10-307-956-23
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPPXY 6
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US-10-307-956-23
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; Publication No. US20030119072A1
; GENERAL INFORMATION:
; APPLICANT: Nie, Weilin
; APPLICANT: Aberia, Merl F.
; APPLICANT: Murray, Brion
; APPLICANT: Merray, Brion
; APPLICANT: Merray, Brion
; APPLICANT: Merray, Brion
; APPLICANT: Merray, Brion
; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
; TITLE OF INVENTION: METHODS 133
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 1999-08-30
; PRIOR FILING DATE: 1999-08-30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SOFTWARE: PastSEQ for Windows Version 3.0
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80.0%; Pred. No. 4.9e+02;
.ive 0; Mismatches 1; Indels
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                   ALLOANDE, CARDER, ALLOANDER: 18,872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 799-9090
TELEFAX: (212) 896-8864/9741
TELEFAX: (212) 896-8864/9741
TELEFAX: (210) 896-8864/9741
TELEFAX: (212) 896-8864/9741
TELEFAX: (213) 896-8864/9741
TELEFAX: (214) 896-8864/9741
TELEFAX: (215) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (10)...(10)
... OTHER THORMATION: Xaa = Leucine or Methionine
US-10-307-956-17
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 140:
US-10-185-050-140
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                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
         ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.vv
A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.v
A; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PPPXY 6
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US-10-307-956-17
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Sequence 170, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Brian K.
Ray, Brian K.
Powikes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: Unknown>
PRIOR APPLICATION PATE:
APPLICATION DATE: 03-APE-1997
                                                                                                                                                                                                                                                                                                                                                                        93.3%; Score 28; DB 14; Length 16; 80.0%; Pred. No. 5.4e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
  REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
STRANDEDNESS: «Unknown»;
TOPOLOGY: unknown
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-10-185-050-170
                                                                                                                                                                                                                                           TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 229:
US-10-185-050-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
                                                              TELEPHONE: (212) 790-9990
TELEFAX: (212) 896-864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 170: SEQUENCE CHARACTERISTICS: LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION
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Best Local Similarity 80.۰۰
نمو 4; Conservative
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STATE: New York
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US-10-185-050-170
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Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                 COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRILING DATE: 03-Apr-1997
ATONEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 996-8664/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.3%; Score 28; DB 14; Length 16; 80.0%; Pred. No. 5.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTEX: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-185-050-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 229, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MISROCK, S. LESLIE
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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Best Local Similarity
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US-10-185-050-229
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RESULT 15
US-10-185-050-171
Sequence 171, Application US/10185050
Sequence 171, Application US/10185050
GENERAL INFORMATION: Gregorio
APPLICANT: Pirozzi, Gregorio
APPLICANT: Pirozzi, Dana M.
Fay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
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ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUTTY: New York
COUTTY: New York
COUNTY: USA
ZIP: 1036-2711
COMPUTER READABLE FORM:
MADLUM TYPE: PLOPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION NUMBER: US/08/826,516
FILING DATE: 03-API-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISSOCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELENCONTUNICATION INFORMATION:
NAME: MISSOCK, S. LESLIE
REGISTRATION NUMBER: 1101-208-999
93.3%; Score 28; DB 14; Length 17; 80.0%; Pred. No. 5.7e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.3%; Score 28; DB 14; Length 17; 80.0%; Pred. No. 5.7e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 171:
US-10-185-050-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 171:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                            4; Conservative
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                              ||| |
PPPAY 12
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Search completed: October 13, 2005, 14:50:02 Job time : 13.7912 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2005, 14:36:01; Search time 2.50549 Seconds (without alignments) 230.414 Million cell updates/sec Run on:

US-09-385-918-15 30 Title: Perfect score:

1 XPPPXY 6 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	cal	٦	_	_		_		ъ.	hypothetical prote		Pex protein [impor	ŧ	ısin class	QID3 protein - fun	hypothetical prote	hypothetical prote	ப	hypothetical prote	cal	conserved hypothet		conserved hypothet		_		Н		hypothetical prote
SUMMARIES	ID	874359	T31844	T31845	3308	T41925	T05386	T44170	T43984	T09318	T33486	E64498	AD2303	W4WLB2	S14970	842579	T29840	D72652	T41481	T39811	F96575	D82755	A29356	H87551	T29641	AC3314	A72638	02	269	56
	DB	2	~	~	~	N	~	7	7	7	7	~	~	7	7	7	~	~	~	N	~	~	~	7	N	~	7	~	7	7
	Length	62	99	70	82	82	85	88	88	93	99	0	ч	ч	132	4	143	4	149	S	ß	S	ø	9	166	9	7	171	7	172
de	당선	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93,3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3
	Score	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
	Result No.	וו	7	m	4	Ŋ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote hypothetical prote	hypothetical prote OmpA family protei	hypothetical prote membrane-bound cyt	hypothetical profe	signal peptidase i pathogenesis-relat		hypothetical prote	blesz procein z nu hypothetical prote	hypothetical prote	hypothetical prote	serine /proline ri
T27505 T18677	T33440 E87601	D70509 S31938	T34104	T04233	G97235	F72579	S33204	T29976	T16654	T37825
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172	178	198	200	210	210	212	222	223	223	224
93.3 93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3	93.3
7 5 8 7 8 8	7 8 8 7 8 8	7 S B S	28	78 78 78	28	5 5 8 6	9 8 7 8	28	28	28
30	332	1 6 6 4 10	36	38	39	0 7	4.4	43	44	45

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Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA, Res. 3, 109-136, 1996
A.fittle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Rossidues: 1-62 «KAN»
A;Cross-references: UNIPROT:P72574; EMBL:D64001; GB:AB001139; NID:g1001102; PIDN:BAA102
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                           C.Species: Synechocystis sp.
A.Variety: PCC 6803
C.Date: 25-Apr.1997 #sequence_revision 25-Apr.1997 #text_change 09-Jul-2004
C.Accession: S74359
hypothetical protein ssr0109 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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ö Gaps .. 0 1; Indels 93.3%; Score 28; DB 2; L 80.0%; Pred. No. 1.1e+02; Live 0; Mismatches 1; Best Local Similarity 80.0 Matches 4; Conservative

20 PPPTY 24 2 PPPXY 6 g ò

hypothetical protein CO2E7.7 - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

Cyaccession: T31844
R/Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, June 1998
A;Description: The sequence of C. elegans cosmid C02E7.
A;Recession: T31844

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-66 <FUL>
A;Residues: 1-66 <FUL>
A;Cross-references: UNIPROT:O16427; EMBL:AF016446; PIDN:AAC24166.1; GSPDB:GN00023; CESP
A;Experimental source: strain Bristol N2; clone CO2E7

A; Gene: CESP: C02E7.7

A; Map position: 5 A; Introns: 29/2

Length 66; 93.3%; Score 28; DB 2; I 80.0%; Pred. No. 1.1e+02; Query Match Best Local Similarity

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C;Accession: T41925

R;Nicholas, J.

B;Nicholas, J.

B;Description: Determination and analysis of the complete nucleotide sequence of human P.

B;Reference number: 222022

B;Reference number: 222022

B;Reference number: 222022

B;Reference number: 222022

B;Reference number: 22002

B;Reference number: D2022

B;Reference number: D32

B;Residues: 1-82 NIC>

B;Residues: 1-82 NIC>

B;Residues: 1-82 NIC>

B;Residues: DNA

B;Residues: 1-82 NIC>

B;Residues: DNA

B;Residues
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R;Bevan, M.; Watson, M.D.; Gibbons, T.; Bartley, J.; Bancroft, I.; Mewes, H.W.; Mayer, R
Bubmitted to the Protein Sequence Database, August 1998
A;Reference number: Z15413
A;Accession: T05386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T44170
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human A;Reference number: Z22734; MUID:99412318; PMID:10482553
A;Accession: T44170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F16G20.180 - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein U24 [imported] - human herpesvirus 6 (strain 229) C; Species: human herpesvirus 6 A; Variety: strain 229 C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #sequence_revision 21-Jan-2000 #sequence_revision 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 82
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A;Cross-references: UNIPROT:081744; EMBL:AL031326
A;Experimental source: cultivar Columbia; BAC clone F16G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; I
Pred. No. 1.4e+02;
0; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-88 <DOM>
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A;Experimental source: strain Z29; variant B
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conseri
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Best Local Similarity
Matches 4; Conserv
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A, Note: F16G20.180
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18189
R;Fulton, B.; Wohldmann, P.
submitted to the EMBL. Data Library, June 1998
A;Description: The sequence of C. elegans cosmid CO2E7.
A;Reference number: Z21093
A;Accession: T31845
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reterence: UNIPROT:O16428; EMBL:AF016446; PIDN:AAC24165.1; GSPDB:GN00023; CESP:A;Experimental source: strain Bristol N2; clone CO2E7
C;Genetics:
A;Gene: CESP:CO2E7.6
A;Anp position: 5
A;Introns: 29/2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31088
R;Goela, D.; Scheet, P.
Submitted to the EMBL. Data Library, May 1998
A;Boescription: The sequence of C. elegans cosmid R12E2.
A;Reference number: Z21281
A;Reference number: Z21281
A;Reference number: Z21281
A;Rolecule type: DNA
A;Reference number: Leg cGOE>
A;Residues: 1-82 cGOE>
A;Residues: 1-82 cGOE>
A;Residues: Leg cGOE>
A;Residues:
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C;Species: human herpesvirus 7
A:Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                Gaps
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Pred. No. 1.2e+02;
0; Mismatches 1; Indels
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80.0%; Pred. No. 1.46+02;
            Indels
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            Mismatches
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            4; Conservative
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-99 < kLis
A;Cross-references: UNIPROT:Q9TZL2; EMBL:AF098985; PIDN:AAC67418.1; GSPDB:GN00020; CESP
A;Experimental source: strain Bristol N2; clone C08G5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A., rason, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science J.J.; 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi, A;Refearence number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64498
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: UNIPROT:Q8YQ56; GB:BA000019; PIDN:BAB75678.1; PID:g17133113; GSPDB:
A;Experimental source: strain PCC 7120
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C;Species: Nostoc sp. PCC 7120
C;Note: Nostoc sp. ptrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2303
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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Pred. No. 1.7e+02;
0; Mismatches 1;
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity
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A;Map position: 2
A;Introns: 30/3; 75/3
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                                                                                                                                                                                                                                                                                        1430thetical protein U24 [imported] - human herpesvirus 6 (strain HST)
C.Species: human herpesvirus 6
C.Species: human herpesvirus 6
C.Species: human herpesvirus 6
C.Species: human herpesvirus 6
C.Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C.Accession: T43984
S.Istejawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa J. Virol. 73, 8053-8063, 1999
A.Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: Z22732; MUID:99412319; PMID:10482554
A;Accession: T43984
A;Accession: T43984
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-88 <1SE>
A;Cross-references: UNIPROT:Q9WT40; EMBL:AB021506; NID:g4995977; PIDN:BAA78245.1; PID:g4
A;Experimental source: strain HST; pop. variant B
C;Genetics:
A;Note: U24
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C;Date: 11-Unn-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Unn-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09318
A;Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu A;Reference number: 216644; MUID:94118404; PMID:8289364
A;Accession: T09318
A;Accession: T09318
A;Accession: T09318
A;Accession: T09318
A;Cocession: T0931
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33486
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Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
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C'Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
C'Accession: T33486
C'Accession: T3486
R'Klinke, W.; Bauer, C.; Morris, M.
A'Description: The sequence of C. elegans cosmid C08G5.
A'Reference number: Z21356
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80.0%;
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Search completed: October 13, 2005, 15:11:18 Job time : 5.50549 secs
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S14970
Cxbecais class I (clone w17-1) - tomato
Cxbecais Lycopersicon esculentum (tomato)
C;Becies: Lycopersicon esculentum (tomato)
C;Becession: S14970
C;Accession: S14970
C;Superfamily: hydroxyproline-rich glycoprotein
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842579
64.02579
C.Species: Trichoderma harzianum)
C.Species: Trichoderma harzianum
C.Species: Trichoderma
C.Species: Trich
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W4WLB2
E4 protein - bovine papillomavirus type 2
C; Species: bovine papillomavirus type 2
C; Species: bovine papillomavirus type 2
C; Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C; Accession: F31169
R; Groff, D.E.; Mitra, R.; Lancaster, W.D.
Submitted to GenBank, May 1988
A; Reference number: A94519
A; Reference number: A94519
A; Reference number: A94519
A; Residues: 1-118 -GRO-A
A; Crossion: F31169
A; Cross-references: UNIPROT: P11301; GB:M20219; GB:M19551; NID:g332996
C; Superfamily: bovine papillomavirus E4 protein
C; Keywords: early protein
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Best Local Similarity
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Score 28; DB 2; Length 143
Pred. No. 2.5e+02;
0; Mismatches 1; Indels
93.3%;
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Query Match 93.3
Best Local Similarity 80.0
Matches 4; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Vesicular glutamace transporcer 1 (Fragment).
Macaca mulatta (Rhesus anacaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
[1]
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Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G
"Arabidopsis thaliana genes expressed in the early compatible
interacion with root-knot nematodes.";
                                                      Q9tz12
Q8ceh0
Q8s5g3
Q7g6h0
Q9bgz7
Q58985
Q6fm10
Q9bbb3
Q9bbb3
Q9bbb3
Q9bbb3
Q9bbb3
 Q7s376
Q6i141
Q748n0
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Pred. No. 2.5e+02;
0; Mismatches 1; Indels
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Vercauteren I.J.R.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ286344; CAB71008.1; -
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Last annotation update)
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[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            ALIGNMENTS
075376
061141
0748N0
0778N0
0972L2
08CEH0
0885G3
0766N0
098GZ7
YF90 METJA
06FMIO
SPAH MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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80.0%;
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 NCBI_TaxID=3702;
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SEQUENCE
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268.842 Million cell updates/sec
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Compugen Ltd
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Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Minimum Maximum Database

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[1] SEQUENCE FROM N.A. Mowak M., Bauer H., Schumacher J., Runke G., Kramer C., Mayr T., Nowak M., Bauer H., Schumacher J., Runke G., Kramer D.S., Schmid B., Imai Y., Talbot W.S., Mullins M.C., Hammerschmidt M. T., Schwid B., Imai Y., Talbot W.S., Mullins M.C., Hammerschmidt M. T., Schwidt M.S., Schwidt M.S., Berlins M.C., Hammerschmidt M.S., Schwidt M.S., Berlins Hamerschmidt M.S., Mallins M.C., Embl., Avi35144; Ani39185.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Cymbidieae; Bromheadilnae;
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Last sequence update)
Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Extensin (Fragment)
Pred. No. 4.5e+02;
0; Mismatches 1;
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80.0%; Pred. No. 5e+02;
iive 0; Mismatches
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NON TER 1 1 1
SEQUENCE 48 AA; 5317 MW;
80.08;
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Matches 4; Conservative
                           4; Conservative
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  Best Local Similarity
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NON TER
SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos tauras (Bovine).
Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Pred. No. 4.4e+02;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                    Score 28; DB 2; Length 25;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                      1; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO16719; AAH16719.1;
Hypothetical protein.
  SEQUENCE FROM N.A.
TISSUE-Medial basal hypothalamus;
Brown A.E., Ojeda S.R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF424810; AAL40244.1; -.
SEQUENCE 25 AA; 2733 MW; 1730048E8674ASF3 CRC64;
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ535318; CAD59473.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 37 AA; 4001 MW; A1EAA3B5B5E6734C CRC64;
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38 AA; 4064 MW; CAE0F5FD241DC202 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Early growth response protein 1 (Fragment).
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                         Query Match
Best Local Similarity
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TISSUE=Blood;
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NCBI_TaxID=9913;
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01-DEC-2001 (
01-DEC-2001 (
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Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Yano M., Jiang J., Gojobori T.;
"The genome sequence and structure of rice chromosome 1.";
EMBL; AP003237; BAB67898.1; -.
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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80.0%;
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80.0%;
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Fulton B., Wohldmann P.;
"The sequence of C. elega
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Best Local Similarity
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                                                                                                                                       64 AA;
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SEQUENCE FROM N.A.
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Sasaki T., Nimurza Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., Hosokawa S., Masukawa M., Zrikawa K., Chiden Y., Hayashi M., Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijina M., Ikeda M., Ikeno M., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y., Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y., Maramima M., Nakamima M., Nakamima M., Nakamima M., Saji S., Sakai, K., Shibata M., Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., Waki K., Yamangata H., Yoshiki S., Yoshihara R., Yukawa K.,
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PCC6803;
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Marsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-0CT-2002 (TrEMBLrel. 22, Last ann
P0046E05.3 protein.
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Best Local Similarity
Matches 4; Conserv
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  PPPXY 6
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Rhabditidae, Peloderinae, Caenorhabditis.
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STRANTHE-BISSOR13:
MEDILINE-99069613; PubMed-9851916;
WormBase Consortium;
WormBase Consortium;
WormBase Consortium;
MormBase Consortium;
MormBase Consortium;
MormBase Sequencie of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
Science 282:2012-2018(1998).
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                                                           Length 64;
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Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO16446; AAC24166.1; -.
PIK; T31844; T31844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston R.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 66 AA; 6077 MW; B393B3D0B8E39915 CRC64;
7001 MW; 8E5A64A20BC656C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
Hypotherical protein C02E7.7.
Name-C02E7.7; ORFNames=C02E7.7;
Caenorhabditis elegans.
                                                        Score 28; DB 2; 1
Pred. No. 7.7e+02;
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STRAIN=Bristol N2;
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88155754; PubMed=2831380; Wagner E.K., Devi-Rao G.B., Feldman L.T., Dobson A.T., Zhang Y.-K., Flanagan W.M., Stevens J.G.; Physical characterization of the herpes simplec virus latency-
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                                                                                                                                                                                                                 Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 2; Length 69;
Pred. No. 8.3e+02;
0; Mismatches 1; Indels
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STRAIN=Bristol N2;
Fulton B., Wohldmann P.;
"The sequence of C. elegans cosmid CO2E7.";
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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STRAND-Bristol N2;
Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7286 MW; 9E26E5B0750DB39A CRC64;
                                                                                                             Q9YPF8;
U-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
Hypothetical protein C02E7.6.
                                                                                       69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated transcript in neurons.",
J. Virol. 62:1194-1202(1988).
EMBL; M17921; AAA45796.1; -
SEQUENCE 69 AA; 7286 MW; 9E26ESF
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MEDLINE=99069613; PubMed=9851916;
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Human herpesvirus 1 (HHV-1) (H
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80.0%;
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Orchidaceae; Spermatophyta, higher Epidendroideae, Cymbidieae, Bromheadilnae,
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
Hypothetical protein OSJNBa0055113.11.
Name=OSJNBa0055113.11;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                       Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AF016446; AAC24165.1; -. EMBL, AF016446; AAC24165.1; -. EMBL, T31845; T31845; T31845; WormBase; WBGeneO0015339; C02E7.6. WormBep; C02E7.6; CE07843. Hypothetical protein SeQUENCE 70 AA, 6547 MW; 9FB8F12AA71C46FD CRC64; SEQUENCE 70 AA, 6547 MW; 9FB8F12AA71C46FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR005648; BAD28928.1;
Hypothetical protein.
SEQUENCE 73 AA; 7920 MW; F3EB1BAF0E1FAICB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lim S.H.,
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 71 AA; 7715 MW; 5FEF6A5483C9DD8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Score 28; DB 2; I
Pred. No. 8.4e+02;
0; Mismatches 1;
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Pred. No. 8.5e+02;
0; Mismatches 1;
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80.0%;
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WormBase Consortium;
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Sasaki T., Matsumo
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NCBI_TaxID=41205;
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Search completed: October 13, 2005, 15:09:26 Job time : 14.4286 secs
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                                         Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryzaa.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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           Score 28; DB 2; Length 73; Pred. No. 8.8e+02;
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                                         1; Indels
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STRAIR=CD-1; TISSUE=Uterus;
Lim H. Das S.K., Dey S.K.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF059177; AAC28334.1;
GD; GO:0045165; P:cell fate commitment; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XNU9; -.
75 AA; 7723 MW; A88ECB2376BB373D CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
EGF-like growth factor receptor ErbB4 intracellular
                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence and analysis of rice chromosome 4.";
93.3%; Scor.
80.0%; Pred. No. e..
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EMBL; AL662950; CAE04335.2; -.
Gramene; Q7XN09; -.
                                         4; Conservative
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Name=OSJNBa0008M17.8;
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Name=Erbb4;
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                                                                        718C044E67673A70 CRC64;
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80.0%; Pred. No. 9e+02;
Live 0; Mismatches
GO; GO:0007507; P:heart development; IMP.
GO; GO:0007399; P:neurogenesis; IMP.
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75 75
75 AA; 8371 MW;
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Best Local Similarity
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GenCore version 5.1.6	27
Copyright (c) 1993 - 2005 Compugen Ltd.	28
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OM protein - protein search, using sw model	31
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Run on: October 13, 2005, 14:01:04; Search time 13.5165 Seconds	33
(without alignments)	34

Scoring table: BLOSHM62	۵		
44	Gapon 10.0 , Gapext 0.5 2105692 segs, 386760381 residues hits satisfying chosen parameters:	2105692	

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 0 length: 2000000000 Beq Beq Minimum DB Maximum DB

geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2004s:\* geneseqp2000s:\* ......... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

, , ,	n Sma	1 PY	Y mot	n Sma	n Sma	n Sma	Biotinyla	motif	motif	motif	n PRO	Hydrophob	n pol		1 hum	n PRO	n sec	n sec	n PRO	n sec	n sec	n PRO	l hum	n PRO	n PRO
uo.	Human	WBP-1	<b>PPPPY</b>	Human	Human	Human	Biot	PY	ΡY m	PY m	Human	Hydr	Human	Human	Novel	Human	Novel	Human	Human						
Description	Aab83031	Aar98323	Aaw38058	Aab83032	Aab83037	Aab83038	Adb49248	Aaw82836	Aaw82840	Aaw82839	Aab24036	Aab12136	Aam93501	Abg34048	Abo00496	Ada01306	Ada43735	Ada43503	Ada01178	Ada01062	Ada43619	Ada06881	Ada08369	Adb99662	Adb86945
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ΩI	AAB83031	AAR98323	AAW38058	AAB83032	AAB8303	AAB83038	ADB49248	AAW82836	AAW82840	AAW82839	AAB24036	AAB12136	AAM93501	ABG34048	ABO00496	ADA01306	ADA43735	ADA43503	ADA01178	ADA01062	ADA43619	ADA06881	ADA08369	ADB99662	ADB86945
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## ALIGNMENTS

Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif; Smad 1; Smad 5. Human Smad 1 and Smad 5 PY motif consensus seguence. AAB83031 standard; peptide; 6 AA 25-JUN-2001 (first entry) WO200116604-A1. Homo sapiens. RESULT 1 

08-MAR-2001.

29-AUG-2000; 2000WO-US023729. 99US-00385918. 30-AUG-1999;

(SIGN-) SIGNAL PHARM INC.

Murray BW, Mercurio FM; Hoekstra MF, Xie W,

WPI; 2001-327913/34.

ģ Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis bevaluating the ability of agents to modulate Smad protein degradation.

Claim 4; Page 35; 75pp; English.

The present sequence is the Smad PY motif consensus sequence. The PY motif binds to the WW domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGP) beta and/or bone morphogenic protein (BMP) mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase wW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular

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        useful for stimulating bone formation in a patient or treating at condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motif (AAR97694) of WBP-1 (AAR97695), a ligand of the WW signalling domain of a novel human proto-oncogene associated protein, YAP (AAR9760). The mutant peptides, which also included the amino acids flanking the PY motif, were expressed as GST fusion proteins in B. coli SURE. Binding to the YAP WW domain was virtually abolished when proline P2 (numbered according to position in the PY motif), p3 or YS was substituted by alanine (AAR997698-700, respectively), and reduced approx. 2-fold when P1 or P4 was altered to alanine (AAR98322-23, respectively)
 The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein - used to modulate treatment of muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A series of mutants (AAR97698-700 and AAR98322-23) was made of the PY
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                    WW domain; signal transduction; diagnosis; gene therapy;
Yes proto-oncogene associated protein; YAP; ligand; WBP-1; PY motif.
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protein HECT E3 ubiquitin ligase activity.
                                                                                                                                           Length 6;
                                                                                                                                                                 0; Indels
                                                                                                                                        100.0%; Score 37; DB 4; I
100.0%; Pred. No. 1.8e+06;
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DELBRUECK CENT MOLECULAR MEDICINE MAX.
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding Yes proto-oncogene associated intracellular signal transduction e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 85; 126pp; English.
                                                                                                                                                                                                                                                                        AAR98323 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00348518.
95US-00476509.
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                                                                                                                                                                                                                                                                                                                                             WBP-1 PY motif (P4A mutant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen H, Bork P;
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-286829/29
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                       TPPPAY
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                                                                                                                   Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYRQ ) UNIV
(DELB-) DELBF
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levels of
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dystrophy
                                                                                                                                                                                                                                                                                               AAR98323;
                                                                                                                                                                 Matches
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Gaps

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containing this rich regions of WBP-1 and WBP-2 proteins. Peptides containing this residue have been shown to bind the YAP ww domain, but not the WW domain from dystrophin or to a panel of SH3 domains. Peptides AMM38057-67 were biotinylated and complexed with alkaline streptavidin, and used in a cross affinity mapping experiment. They were tested for their ability to bind to the 12 individual novel WW domains of WWP1 (AAM36794), WWP2 (AAM36795), WWP3 (AAM37696) and WWP4 (AAM36797), which were expressed as glutathione-S-transferase expression proteins. The present peptide is derived from WBP-1, and binds to some of the WW domains of the novel proteins. The WW domain is a small functional domain. Its name is derived from the observation that two tryptophan cenidues, one in the amino terminal portion of the WW domain and one in the carboxyl terminal portion, are conserved. Most proteins containing WW domain shave a function involving cell signalling and growth regulation of the organisation of the cytoskeleton. Polypeptides containing a WW domain are identified by treating a multivalent recognition unit complex that has selective binding affinity for a WW domain, with many the complex. Proteins containing WW domains are used for targeted drug complex. Proteins containing WW domains are used for targeted drug complex. Proteins containing WW domains are used for targeted drug complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide recognition unit; WW domain; cell signalling; growth regulation; cytoskeleton organisation; targeted drug screening; modulator; WW domain interaction; YAP protein; dystrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying cell signalling and growth regulatory polypeptides by reaction with multivalent recognition complex - polypeptides are useful in targetted drug selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides AAW38057-67 contain PPPPY-like motifs. The PPPY motif is found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPPY motif containing peptide used to bind WW domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 15A; 220pp; English.
                                                                                                                                                                                                                                                      AAW38058 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay BK, Fowlkes DM;
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                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998 (first entry)
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TPPPAY
                                                                     TPPPAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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The present sequence is a Smad PY motif consensus sequence. The PY motif binds to the WM domain of HBCT (homologous to BG carboxyl terminus) E3 ubiquitin ligase. resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGP)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insulficient TGP-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for treating inflammation, broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGP-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                                                                                                                                                    Human; HECT; homologous to B6 carboxyl terminus; ubiquitination; HECT B3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; againg; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif; Smad 1; Smad 5.
                                                                                                                                                                                                                                              Human Smad 1 and Smad 5 PY motif consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercurio FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                      AAB83032 standard; peptide; 14 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murray BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Leu, Met
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Best Local Similarity 10v...
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TPPPAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                        25-JUN-2001
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                                                                                                                                                              AAB83032;
                                                                                                     AAB8303
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Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                       Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif.
                                                                                                                                                                                                                                                                                                                                                                        Mercurio FM;
                                                                   AAB83037 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 29; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Murray BW,
                                                                                                                                                                                                                                                                                                      29-AUG-2000; 2000WO-US023729
                                                                                                             25-JUN-2001 (first entry)
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                                                                                                                                   Human Smad PY motif
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TPPPAY
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                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                        AAB83037;
                                             RESULT 5
AAB83037
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protein bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or EMPP-mediated cell signalling. Agents that inhibit EMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment EMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis The present sequence is a Smad PY motif. The PY motif binds to the WW domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for similating

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Sequence 14 AA;
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Similarity 100.0%; Score 37; DB 4; Length 14; Similarity 100.0%; Pred. No. 31; 6; Conservative 0; Mismatches 0; Indels
          Local Similarity
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Matches
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Gaps .

Indels

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0; Mismatches

100.0%; Score 37; DB 4; Length 14; 100.0%; Pred. No. 31;

(first entry)

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WW domain; drug candidate screening; drug discovery; drug modification; drug refinement; immunogen; WW binding protein; WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified polypeptide comprising WW domain, useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological activities, or as an immunogen to generate
                                                                                  Biotinylated WW domain binding peptide #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example, Fig 15A; 133pp; English.
                                                                                                                                                                                                                                                                                                                                 28-JUN-2002; 2002US-00185050.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAYB/) KAY B K.
(FOWL/) FOWLKES D M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-635075/60.
                                                                                                                                                                                                                                            US2003077577-A1.
                                                                                                                                                                                                   Unidentified.
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                                           04-DEC-2003
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ADB49248;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (PIRO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a Smad PY motif. The PY motif binds to the WW domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase, resulting in ubiquitation of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP)-mediated signalling. The method involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase, or on the cellular levels of Smad protein hECT E3 ubiquitin ligase, or on the cellular levels of Smad protein hECT E3 ubiquitin ligase, or so the cellular levels of Smad protein hECT E3 ubiquitin ligase, or superior is useful for stimulating bone formation in a patient or treating a condition associated with inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for treating cancer, that inhibit TGF-mediated signalling are useful for treating cancer, that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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                                                                                                                                                                                                                     Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMF; Smad; cell signalling; inflammation; againg; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif.
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                                           AAB83038 standard; peptide; 14 AA.
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100.0%;
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                                                                                                                                (first entry)
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                                                                                                                                                                              Human Smad PY motif #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-327913/34.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1999;
                                                                                                                                  25-JUN-2001
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                                                                                       AAB83038;
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Matches
  RESULT 6
                         AAB83038
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Fowlkes DM;

Кау ВК,

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96US-00630916. 97US-00826516.

PIROZZI G.

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The invention describes a purified polypeptide (I) comprising a WW domain which has a sequence (S1) selected from 11 sequences fully defined in the specification, a sequence (S2) selected from 48 sequences fully defined in the specification or a sequence (S3) comprising 683, 906, 224 or 725 amino acids fully defined in the specification (I) is useful for screening a potential drug candidate, by allowing (I) to come into contact with at least one recognition unit having a selective affinity for the WW domain in (I), in the presence of an amount of a potential drug candidate, such that (I) and the recognition unit are capable of interacting when brought into contact with one another in the absence of the drug candidate, and determining the effect, if any, of the presence of the amount of the drug candidate on the interaction of (I) with the recognition unit. (I) is useful for drug discovery, modification and refinement, for discovering polypeptides involved in pharmacological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activities, or as an immunogen to generate antibodies. This is the amino acid sequence of a Ww domain binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 37; DB 7; Length 14; 100.0%; Pred. No. 31; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PY motif of the human MAD-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW82836 standard; peptide; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TPPPAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW82836;
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1D AAW8

XX AAW8

AC AAW8

XX O1-F

XX O1-F

XX XX
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ADB49248 standard; peptide; 14 AA.

ADB49248 ID ADB4 XX

1 TPPPAY TPPPAY

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WPI; 1998-583204/49
                                                                                                                                                                                                                                                                                                                                                            Sequence 16 AA;
                             10-APR-1998;
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    15-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-0CT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gimeno CJ,
                                                                                                Gimeno CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW82839;
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                            The present sequence represents the PY motif of a MAD-1 (mothers against dpp (decapentaplegic)) protein. The specification describes a human endothalial MAD interactor 1 protein EM11. The protein modulates transforming growth factor-beta (TGF-beta) responsive cells. The EM11 protein is used to treat EM11 deficiency. They are especially used for treatment of cardiovascular disease (specifically atterossis but also ischaemia/reperfusion, hypertension, restenosis and arterial inflammation) or proliferative diseases, especially cancer of gut-derived cells, e.g. colorectal or pancreatic cancer, also to modulate angiogenesis, treat autoimmune disease or fibrosis and to
                                                                                                                                                                                                                                                                         Nucleic acid encoding endothelial MAD interactor I - for modulating cell proliferation and differentiation, e.g. in cases of atherosclerosis and
Endothelial MAD interactor protein 1; mothers against dpp; MAD-1; decapentaplegic, human; transforming growth factor-beta; TGF-beta; EMI1 deficiency; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; arterial inflammation; proliferative disease; cancer; colorectal; pancreatic; antisense; anglogenesis; autoimmune disease; fibrosis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endothelial MAD interactor protein 1; mothers against dpp; MAD; decapentaplegic; human; transforming growth factor-beta; TGF-beta; EMI1 deficiency; cardiovascular disease; atherosclerosis; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reperfusion; hypertension; restenosis; arterial inflammation; proliferative disease; cancer; colorectal; pancreatic; antisense; anglogenesis; autoimmune disease; fibrosis; wound healing.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 37; DB 2; Length 16; 100.0%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PY motif of the Drosophila MAD protein.
                                                                                                                                                                                                                                                                                                                       Example 4; Page 67; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82840 standard; peptide; 16 AA.
                                                                                                                                                                              97US-00844312
                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                cancer of colon or pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulate wound healing
                                                                                                                                                                                                                            Falb DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TPPPAY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orosophila sp
                                                                                  Homo sapiens.
                                                                                                          WO9845467-A1.
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                                                                                                                                                                                                                           Gimeno CJ,
                                                                                                                              15-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW82840;
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                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding endothelial MAD interactor I - for modulating cell proliferation and differentiation, e.g. in cases of atherosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial MAD interactor protein 1; mothers against dpp; Smad-5; decapentaplegic; human; transforming growth factor-beta; TGF-beta; EMIl deficiency; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; atterial inflammation; proliferative disease; cancer; colorectal; pancreatic; antisense; anglogenesis; autoimmune disease; fibrosis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 37; DB 2; Length 16; 100.0%; Pred. No. 35; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 67; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW82839 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PY motif of the Smad-5 protein.
98WO-US007356
                                                                      97US-00844312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US007356
                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer of colon or pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1999 (first entry)
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                                                                                                                                                                                                                                                                                                   WPI; 1998-583204/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Falb DA
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Best Local Similarity
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Matches
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                                                                     The present sequence represents the PY motif of a Smad-5 (mothers against dpp (decapentaplegic)) protein. The specification describes a human endothalial MAD interactor 1 protein EMI1. The protein modulates transforming growth factor-beta (TGF-beta) responsive cells. The EMI1 protein is used to treat EMI1 deficiency. They are especially used for treatment of cardiovascular disease (specifically atheroscierosis but also ischaemia/reperfusion, hypertension, restenosis and arterial inflammation) or proliferative diseases, especially cancer of gut-derived cells, e.g. colorectal or pancreatic cancer, also to modulate angiogenesis, treat autoimmune disease or fibrosis and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
          Nucleic acid encoding endothelial MAD interactor I - for modulating cell proliferation and differentiation, e.g. in cases of atherosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an antibody that binds to a human protei (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434; PRO1927; PRO1927; PRO4364; PRO4394; PRO4364; PRO4397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibodies specific for PRO polypeptides, used to diagnose and inhibit the growth of tumors in mammals, and to identify inhibitors of PRO polypeptide activity or expression.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour; diagnosis; neoplastic disease; proliferation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe CK,
                                                                                                                                                                                                                         Score 37; DB 2; Length 16; Pred. No. 35;
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                identification; tumourigenesis; anticancer; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO4407 protein sequence SEQ ID NO:47.
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL,
                                                                                                                                                                                                                                                                                                                                                 AAB24036 standard; protein; 216 AA
                                                    Example 4; Page 67; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 61; Fig 32; 226pp; English.
                                                                                                                                                                                                                           100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US020111.
99US-0162506P.
99WO-US028313.
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                                cancer of colon or pancreas.
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goddard A,
                                                                                                                                                                                   regulate wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-594320/56.
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
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TPPPAY 12
                                                                                                                                                                                                                                                                      TPPPAY 6
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                                                                                                                                                                                                         Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200053750-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                      AAB24036;
                                                                                                                                                                                                                                                                                                                             RESULT 11
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                              activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC5812 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58013 to AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrophobic domain protein from clone HP10625 isolated from Liver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 37; DB 3; I
100.0%; Pred. No. 3.8e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12136 standard; protein; 216
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98JP-00364315.
99JP-00069811.
99JP-00119299.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hemostatic, thrombolytic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 216 AA;
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27-APR-1999;
19-MAY-1999;
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(PROT-)
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Query Match
Best Local Similarity
     Sequence 216 AA;
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05-SEP-2000;
22-SEP-2000;
10-NOV-2000;
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03-APR-2001;
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                                                                                                                                                                                                                                                                    ABG34048;
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                                                                           Matches
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cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is a human protein which has at least one hydrophopic domain. This protein may be a secretory or a membrane protein. The present protein may have cytokine and cell proliferationalization activity, immune stimulating or suppressing activity, haematopoiesis activity, issue growth activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, anti-inflammatory activity haemour inhibition activity. The present protein could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830 Primers useful for synthesizing full length cDNA clones and their use
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                Query Match 100.0%; Score 37; DB 3; Length 216; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 6; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM93501 standard; protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide, SEQ ID NO: 3209
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02-MAY-2000; 2000JP-00183765
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                                                                                                                                                                                disease, and cancer
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                                                                                                                                                                                                                 Sequence 216 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the cDNA and protein sequences of novel secreted and transmembrane polypeptides PRO polypeptides. The invention also comprises a method for producing the proteins of the invention by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; PRO; secreted protein; transmembrane protein; genetic disorder;
                                                     Gaps
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Wood WI, Zhang Z;
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  Length 216;
100.0%; Score 37; DB 4; I 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0;
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Watanabe CK,
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Stephan J, W
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16-JAN-2001; 2001US-0261939P.

16-JAN-2001; 2001US-0261939P.

25-JAN-2001; 2001US-0264395P.

02-FEB-2001; 2001US-0266421P.

09-FEB-2001; 2001WO-US006520.
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2000US-0235147P.
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01-JUN-2001; 2001WO-US017800.
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                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Human Pro peptide #19.
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Smith V,
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N-PSDB; ABK69979.
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invention. The antibodies specific for the protein of the invention. The antibody may be used for detecting the PRO proteins of the invention and may be used to modify their activity. Polymorleotides may be used as hybridisation probes for a cDNA library to isolate the full-length PRO cDNA or to isolate other CDNAs, to construct hybridisation probes for mapping the gene which encodes that PRO and for genetic probes for mapping the gene which encodes that PRO and for genetic other proteins or molecules involved in binding reaction, to generate transgenic animals or knock-out animals which in turn are useful in the transgenic animals or knock-out animals which in turn are useful in the cheromore identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect of conditionance in the proposes of the sequences may also be used to detect for differentially expressed genes using microarray technology. The present sequence represents a human PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 216 AA;
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100.0%; Score 37; DB 5; Length 216; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Then 6; Conservative 190 TPPPAY 195 1 TPPPAY 6 ò g

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Gaps

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ABO00496 standard; protein; 216 AA. Novel human polypeptide #83 (first entry) 06-AUG-2003 

Human, angiogenesis, cytokine, cell proliferation, pluripotent; cell differentiation; bio-sensor, neuroepithelial cell; autoimmune disease; neural cell; genetic disorder; nerve; brain tissue; central nervous system disease; peripheral nervous system disease, neuropathy; haematopoiesis; bone; myeloid disorder; lymphoid cell disorder; platelet disorder; tendon; regeneration; cartilage; tendon; ligament; nerve tissue growth; tissue repair; wound healing; burn; ulcer; osteoporosis; cancer; osteoarthritis; bone degenerative disorder; periodontal disease; gut protection; lung fibrosis; liver fibrosis; reperfusion injury; thrombolysis; thrombolysis; coagulation disorder; hereditary disorder; blorbythm; circadian cycle; fertility; metabolism; anabolism; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; haemostatic; vulnerary; antiulcer; osteopathic; antiarthritic; vasotropic; immunostimulant; antibacterial; fungicide; immunosuppressive; antirheumatic; antidiabetic; antiasthmatic; cytostatic; virucide.

Homo sapiens.

WO2003023013-A2

20-MAR-2003.

13-SEP-2002; 2002WO-US029001

13-SEP-2001; 2001US-0322511P. 12-SEP-2002; 2002US-00243552.

(HYSE-) HYSEQ INC.

Ma Y; Ö Weng Yang Y, Wang Z, Tang YT,

WPI; 2003-313249/30. N-PSDB; ACD05573.

Comprehensive and their renording polypeptides. The novel polypeptides exhibit activities relating to angiogenesis, cytokine, cell polypeptides exhibit activities relating to angiogenesis, cytokine, cell prolypeptides are involved in the prolypeptides are involved in the coroliferation, differentiation, antification, differentiation and survival of pluripotent and toripotent proliferation, differentiation and survival of pluripotent and toripotent ten cells, and are useful for re-engineering damaged or diseased tissues, transplantation, manufacture of the oppopulates include the stem cells in culture to give rise to neuroepithalal cells that can be used to angment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptides and bean to proliferation of neural cells and regeneration of nerve and bean in tissue and neuropathias, such as Alzheimer's, Farkinson's disease, anyorivorphic lateral scleroais (ALS). The polypeptides are also involved in chemocracic or chemokines activity, regulation of hemmeropoiesis and are useful for the treatment of central and peripheral nervous system which is the properties of the properties, such as Alzheimer's, Farkinson's disease, anyorivorphic lateral scleroais (ALS). The polypeptides are also involved in chemocracic or chemokined; carbory or regulation of hemmeropoiesis and are useful for treating operation of bone, cartilage, tendon, ligament and/or nerve tissue growth, in tissue repair, healing of burns, incisions, ulcers for cregeneration and treatment of lung or liver fibrosis, repetitions and inciding severe combined immunodeficiency (SID) bacterial or fungal in conditions, such as asthma or order respiratory problems. The polypeptides are involved in thromolysis or thrombosis and are useful in treatment of various capallation disorders (sinchiding severe combined immunodeficiency (SID) bacterial or fungation and anabolism, and anabolism, and anebolism, and anabolism, and anebolism, and anebolism, and anebolism, and ana Novel nucleic acids and polypeptides for diagnosis, treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic present invention relates to the isolation of novel human ftp.wipo.int/pub/published\_pct\_sequences Claim 20; SEQ ID NO 419; 300pp; English lateral sclerosis. The 

Sequence 216 AA;

Gaps .; 0 100.0%; Score 37; DB 6; Length 216; 100.0%; Pred. No. 3.8e+02; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 6; Conservative Query Match

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190 TPPPAY 195 1 TPPPAY 6 ò g Search completed: October 13, 2005, 15:00:36 Job time : 15.5165 secs Sequence 13, Appl Sequence 14, Appl Sequence 4, Appli Sequence 37020, A Sequence 52237, A Sequence 7, Appli Sequence 7, Appli Sequence 52237, A

Appli Appli

Sequence Sequence

4, 6, 6, 9519, 6, Appli

Sequence 2, Al Sequence 13, Al Sequence 14, Al Sequence

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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APPLICANT: BEER, BORK
APPLICANT: PEER, BORK
APPLICANT: PEER, BORK
TITLE OF INVENTION: SIGNALLING DOMAIN THERBIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PICTURE OF INVENTION: PROTEIN AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 37; DB 3; Length 10; 100.0%; Pred. No. 2.7; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PROPER FLOPS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
US-09-438-185A-243

US-09-354-221-4

US-08-817-436A-2

US-08-844-312-13

US-08-844-312-14

US-08-844-4

US-08-752-844-4

US-09-192-838B-4

US-09-324-191-4

US-09-324-191-4

US-09-324-191-4

US-09-324-191-4

US-09-270-767-37020

US-09-270-767-37020

US-09-270-767-37020

US-09-270-767-37020

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US-08-663-56A-5

US-08-23-610-5
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                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/476,509B
01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                             US-08-476-509B-35; Sequence 35, Application US/08476509B Patent No. 6034212; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REPRENCE/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
    MOLECULE TYPE: peptide HYPOTHETICAL: NO US-08-476-509B-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
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      Sequence 1013. A Sequence 10865, A Sequence 10865, A Sequence 11, Appl Sequence 14, Appl Sequence 13, Appl Sequence 9, Appli
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6393, Ap
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                                                                                                          October 13, 2005, 13:50:53; Search time 2.85714 Seconds (without alignments) 156.763 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15,
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Sequence
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                                                                                                                                                                                                                                                                                                                   513545
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(/ggn2 6/ptodata1/iaa/5A COMB.pep:*

(/ggn2 6/ptodata1/iaa/5B COMB.pep:*

(/ggn2 6/ptodata1/iaa/6A COMB.pep:*

(/ggn2 6/ptodata1/iaa/6B COMB.pep:*

(/ggn2 6/ptodata1/iaa/6B COMB.pep:*

(/ggn2 6/ptodata1/iaa/PCTUS COMB.pep:*

(/ggn2 6/ptodata1/iaa/backfiles1.pep:*
                     5.1.6
Compugen Ltd
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US-09-198-452A-254
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                                                                                                                                                                                                                                                                                  513545 segs, 74649064 residues
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                     GenCore version (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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Match Length
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465
475
492
77
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Gaps

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PELENSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-013
TELECHONE: (617)227-7400
TELECHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: S.1.veri, Jean M.
REGISTRATION NUMBER: 39,030
REPRENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 6, Conservative
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MOLECULE TYPE: peptide

US-08-844-312-12
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STATE: Massachusetts
COUNTRY: USA
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APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: Kay, Brian K.
APPLICANT: FOWLKS: Dana M.
TITLE OF INVENTION: DENTRICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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WS-09-844-312-12

Sequence 12, Application US/08844312

Patent No. 5948639

GENERAL INFORMATION:

APPLICANT: Carlos J. Gimeno and Dean A. Falb

TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway Genes

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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-haq 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New YORK

COUNTRY: United States

ZIP: 10036-271

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RE-BASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,916A

FILING DATE: 03-APR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MISROCK, S. LESLIE

REGISTRATION NUMBER: 18,072

REGISTRATION NUMBER: 1101-203

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (212) 790-9090

TELEPAX: (212) 790-9090

INFORMATION FOR INFORMATION SEQ ID NO: 54:
                                                                                                                             US-08-630-916A-54; Sequence 54, Application US/08630916A; Patent No. 6011137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109-1875
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TPPPAY 8
TPPPAY 6
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                                  TPPPAY 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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Sequence 15. Application US/08844312

| Sequence 15. Application US/08844312
| Patent No. 5948639
| GENERAL INPOMATION:
| TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway Genes
| NUMBER OF SEQUENCES: 16
| NUMBER OF SEQUENCES: 16
| ADDRESSEBE: LAHIVE & COCKFIELD, LLP
| STREET: 60 State Street, Suite 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/844,312
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
FILING DATE:
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APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FITLE OF INVENTION: Myxococcus CURROR FILL S8-10(15849) B CURROR FILLING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILLING DATE: 2000-07-10 PRIOR FILLING DATE: 2000-07-10 SEQ ID NOS: 16825 LENGTH: 128
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                                                                                                                                                                                                                                       100.0%; Score 37; DB 4; Length 128; 100.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/08840767B
Patent No. 6255464
GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Ringlins, Gregory J.
APPLICANT: Thiagalingam, Sam
TITLE OF INVENTION: MAD-Related Genes in the Human
FILE REPERENCE: 01107.05548
CURRENT APPLICATION NUMBER: US/08/840,767B
CURRENT FILING DATE: 1997-04-16
FALLER APPLICATION NUMBER: 60/015,823
FARLIER PILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                      TYPE: PRT
CRGANISM: Myxococcus xanthus
US-09-902-540-10130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6, Conservative
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Best Local Similarity
6, Conservé
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                                                                                                                                                                                                                                                                                                         1 TPPPAY 6
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-10865
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US-08-840-767-43
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US-08-844-312-16
Sequence 16, Application US/08844312
Sequence 16, Application US/08844312
Fatent No. 5948639
Fatent No. 5948639
Fatent No. 59486399
FITLE OF INVENTION:
FITLE OF INVENTION:
FORESPONDENCE: 16
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
FATENCE OF SEQUENCES: 16
STREET: 60 State Street, Suite 510
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                                                                                  100.0%; Score 37; DB 2; Length 16; 100.0%; Pred. No. 4.2;
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COMPUTER READABLE FORM:

MEDLIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/844,312

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                       0; Mismatches
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Patent No. 6833447
GRNERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: S11veri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-
TELECHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 16 amino acids
amino acid
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Matches 6; Conservative
                                                                                                                       6; Conservative
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                 TOPOLOGY: linear
MOLECULE TYPE: peptide
     amino acid
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                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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TPPPAY 12
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                                          ; MOLECULE II
US-08-844-312-15
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APPLICATION NUMBER: US/08/580,031A
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US-08-701-582D-13
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APPLICANT: Graff, Jonathan M.
APPLICANT: Woolf, Tod M.
APPLICANT: Jin, Ping
APPLICANT: Jin, Ping
APPLICANT: Melton, Douglas A.
TITLE OF INVENTION: The "signalin" Family of TGFb Signal
TITLE OF INVENTION: Transduction Proteins, and Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                            100.0%; Score 37; DB 3; Length 455; 100.0%; Pred. No. 1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Kiggins, Greneth W.
APPLICANT: Riggins, Gregory J.
APPLICANT: Thiagalingam, Sam
TITLE OF INVENTION: MAD-Related Genes in the Human; TILE REPERSUCE: 01107.05548
CURRENT FILING DATE: 1997-04-16
EARLIER PILING DATE: 1997-04-16
EARLIER FILING DATE: 1997-04-16
EARLIER FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/08840767B Patent No. 6255464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08580031A Patent No. 6428977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                        6; Conservative
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                                                             ; TYPE: PRT
; ORGANISM: D. melanogaster
US-08-840-767-43
                                                                                                                                                                                                                                                                      220 TPPPAY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 TPPPAY 225
                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                 1 TPPPAY 6
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-580-031A-14
                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-08-840-767-11
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                   SEQ ID NO 43
LENGTH: 455
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                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 37; DB 4; Length 464; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08701582D
Patent No. 6017755
GENERAL INFORMATION:
APPLICANT: WRANA, Jeffrey
APPLICANT: ATTISANO, Liliana
APPLICANT: SCHERE, Stephen W.
TITLE OF INVENTION: MARZ TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,582D
FILING DATE: APAUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
FILING DATE: 20-DEC-1994
CLASSIFICATION: 536
ATTONNEY, AGENT INPORMATION:
NAME: VINCENT, MACTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE, DOCKET NUMBER: 0NV-019.01
TELEPHONE: (617)832-1000
ITELEPHONE: (617)832-1000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanek
REGISTRATION NUMBER: 30.427
REFERENCE/DOCKET NUMBER: 024916-004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID 00: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.vv
G; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                     amino acid
GY: linear
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Gaps
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                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 37; DB 3; Length 465; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-04-767-48

Sequence 48, Application US/08840767B

Sequence 48, Application US/08840767B

Sequence 48, Application US/08840767B

GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Rigaling, Gregory J.
APPLICANT: Rigalingam, Sam
TITLE OF INVENTION: MAD-Related Genes in the Human
FILE OF INVENTION: WAD-Related Genes in the Human
CURRENT APPLICATION NUMBER: US/08/840,767B

CURRENT APPLICATION NUMBER: 60/015,823

EARLIER APPLICATION NUMBER: 60/015,823

EARLIER FILING DATE: 1996-04-18

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FREUSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/08840767B
; Sequence 52, Application US/08840767B
; Patent No. 6255464
; GENERAL INFORMATION:
; APPLICANT: Wogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Rigaling Gregory J.
; APPLICANT: Thiagaling am, Sam
; TITLE OF INVENTION: MAD-Related Genes in the Human
; FILE REFERENCE: 01107.05548
; CURRENT APPLICATION NUMBER: US/08/840,767B
; CURRENT FILING DATE: 1997-04-16
; EARLIER APPLICATION NUMBER: 60/015,823
; SOFTWARE: FASLSEQ for Windows Version 3.0
CURRENT APPLICATION NUMBER: US/08/840,767B
CURRENT FILING DATE: 1997-04-16
EARLIER APPLICATION NUMBER: 60/015,823
EARLIER FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-08-840-767-48
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LENGTH: 465
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                                                                                                                                       NSO-063-893A-19
Sequence 19, Application US/09063893A
Sequence 19, Application US/09063893A
Sequence 19, Application US/09063893A
Sequence 19, Application US/09063893A
THEORY Kenji OKAZAKI et al.
TITLE OF INVENTION: A NOVEL SIGNAL TRANSDUCTION FACTOR AND A TITLE OF INVENTION: GENE ENCODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSE: ABDRESSE: Wendercht, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 465;
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Patent No. 6255464
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Riggins, Gregory J.
APPLICANT: Thiagalingam, Sam
TITLE OF INVENTION: MAD-Related Genes in the Human
FILE REFERENCE: 01107.05548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: WOTDERFORD
SOFTWARE: WOTDERFORD
SOFTWARE: WOTDERFORD
SOFTWARE: WOTDERFORD
APPLICATION NUMBER: US/09/063,893A
FILING DATE: April 22, 1998
CLASSIFICATION DATA:
PRILING DATE: APPLICATION DATA:
FILING DATE: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Chang
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mus musculus
; STRAIN: Swiss-Webster/NIH
US-09-063-893A-19
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 TPPPAY 227
                                                222 TPPPAY 227
  1 TPPPAY 6
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; ORGANISM: Homo sapiens
US-08-840-767-52
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Query Match 100.0%; Score 37; DB 3; Length 465; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

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1 TPPPAY 6 |||||| 221 TPPPAY 226

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Search completed: October 13, 2005, 14:03:07 Job time : 3.98214 secs

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Sequence Sequence Sequence Sequence Sequence Sequence

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APPLICANT: HOEKELTA, MET F.
APPLICANT: HOEKELTA, WEILIN
APPLICANT: Marray, Brion
APPLICANT: Marray, Brion
APPLICANT: Marray, Brion
APPLICANT: Marcurio, Frank
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 860098.433
FILE REFERENCE: 860098.433
FILE REFERENCE: 2002-12-02
PRIOR APPLICATION NUMBER: US/09/385,918
PRIOR APPLICATION NUMBER: US/09/385,918
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
US-10-245-103-38
US-10-245-107-38
US-10-245-107-38
US-10-245-851-38
US-10-245-851-38
US-10-245-851-38
US-10-236-183-38
US-10-238-183-38
US-10-238-183-38
US-10-245-730-38
US-10-245-730-38
US-10-245-730-38
US-10-245-730-38
US-10-245-730-38
US-10-245-851-38
US-10-245-851-38
US-10-245-8621-38
US-10-245-105-38
US-10-245-105-38
US-10-245-105-38
US-10-245-105-38
US-10-245-105-38
US-10-245-105-38
US-10-245-105-38
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US-10-237-636-38
US-10-238-325-38
US-10-238-346-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10307956 Publication No. US20030119072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-10-307-956-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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 RESULT 1
US-10-307-956-16
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Best Local S:
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6
TYPE: PRT
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Sequence 54, Appl
Sequence 17, Appl
Sequence 22, Appl
Sequence 23015,
Sequence 281015,
Sequence 31853, A
Sequence 31853, A
Sequence 38, Appl
Sequence 38, Appl
                                                                                                             ; Search time 12.7912 Seconds (without alignments) 195.471 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUDLISHER APPLICATIONS ANT.

11. (cgn2_6/ptodata1/)/pubpaa/US07_PUBCOMB.pep:*

12. (cgn2_6/ptodata1/)/pubpaa/US07_NEW_PUB.pep:*

13. (cgn2_6/ptodata1/)/pubpaa/US06_PUBGOMB.pep:*

14. (cgn2_6/ptodata1/)/pubpaa/US07_NEW_PUB.pep:*

15. (cgn2_6/ptodata1/)/pubpaa/US07_NEW_PUB.pep:*

16. (cgn2_6/ptodata1/)/pubpaa/US08_PUBCOMB.pep:*

17. (cgn2_6/ptodata1/)/pubpaa/US08_PUBCOMB.pep:*

18. (cgn2_6/ptodata1/)/pubpaa/US08_PUBCOMB.pep:*

19. (cgn2_6/ptodata1/)/pubpaa/US08_PUBCOMB.pep:*

10. (cgn2_6/ptodata1/)/pubpaa/US08_PUBCOMB.pep:*

11. (cgn2_6/ptodata1/)/pubpaa/US09_NEW_PUB.pep:*

12. (cgn2_6/ptodata1/)/pubpaa/US09_NEW_PUB.pep:*

13. (cgn2_6/ptodata1/)/pubpaa/US09_NEW_PUB.pep:*

14. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

15. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

16. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

17. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

18. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

19. (cgn2_6/ptodata1/)/pubpaa/US10B_PUBCOMB.pep:*

10. (cgn2_6/ptodata1/)/pubpaa/US11_NEW_PUB.pep:*

11. (cgn2_6/ptodata1/)/pubpaa/US11_NEW_PUB.pep:*

12. (cgn2_6/ptodata1/)/pubpaa/US11_NEW_PUB.pep:*

13. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*

14. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*

15. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*

16. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*

17. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*

18. (cgn2_6/ptodata1/)/pubpaa/USS1_NEW_PUB.pep:*
                  5.1.6
Compugen Ltd
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US-10-185-050-54
US-10-307-956-17
US-10-307-956-23
US-10-307-956-23
US-10-424-599-2833015
US-10-767-701-48923
US-10-767-701-359021
US-10-245-115-359021
US-10-245-859-38
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                                                                                                                                                                                                                                                                                              1859788 segs, 416717961 residues
                    version :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                   October 13, 2005, 13:59:34;
                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                protein search, using sw model
                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                  GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                             US-09-385-918-16
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Match 1
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Post-processing:

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Perfect score:

Sequence:

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Run on:

Scoring table:

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TPPPAY

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26 4 3 9 7 8 9 11 10 9 8 11 11

Score

Result 8 2 RESULT

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Gaps

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APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Mie, Weilin
APPLICANT: Mierray, Brion
APPLICANT: Mercurio, Frank
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
TITLE OF INVENTION UNMBER: US/10/307,956
CURRENT APPLICATION NUMBER: US/09/385,918
FRIOR APPLICATION NUMBER: US/09/385,918
FRIOR PLING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hocketra, Merl F.
APPLICANT: Xie, Weilin
APPLICANT: Sie, Weilin
APPLICANT: Mirray, Brinn
APPLICANT: Mirray, Brinn
APPLICANT: Mirray, Brinn
APPLICANT: Mirray, Brinn
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
FILE REFERENCE: 860098.433
CURRENT APPLICATION NUMBER: US/10/307, 956
CURRENT FILING DATE: 2002-12-02
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: RestSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 14
                                                                                                                                                                                                                                                                                                Length 14;
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                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                          100.0%; Score 37; DB 14; Similarity 100.0%; Pred. No. 41; 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                           LOCATION: (10)...(10)
CTHER INFORMATION: Xaa = Leucine or Methionine US-10-307-956-17
                       SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 17 LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/10307956; Publication No. US20030119072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-307-956-22; Sequence 22, Application US/10307956; Publication No. US20030119072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapien
US-10-307-956-22
                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                       NAME/KEY: VARIANT
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US-10-185-050-54
; Sequence 54, Application US/10185050
; Publication No. US2003007757741
; GENERAL INFORMATION:
; APPLICANT: Pirozi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/10307956

Publication No. US20030119072A1

GENERAL INFORMATION:

APPLICANT: Hoekstra, Merl F.

APPLICANT: Ate, Wellin

APPLICANT: Murray, Brion

APPLICANT: Murray, Brion

APPLICANT: Mercurio, Frank

TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL

TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL

TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS

FILE REFERENCE: 860098-433

CURRENT APPLICATION NUMBER: US/10/307,956

CURRENT PILLING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: US/09/385,918

NUMBER OF SEQ ID NOS: 32
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ZIP: 10036-2711

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/185,050

FILING DATE: 28-Jun-2002

CLASSIFICATION: AUNROWN>

PRIOR APPLICATION NUMBER: US/08/826,516

FILING DATE: 03-Apr-1997

ATTORNEY/AGENT INFORMATION:

NAME: MISROCK, S. LESLIE

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-208-999

TELECOMMUNICATION NUMBER: 1101-208-999

TELECOMMUNICATION NUMBER: 1212) 790-9090

TELECOMMUNICATION NUMBER: 1213 896-8864/9741

TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 37; DB 14; Length 14; 100.0%; Pred. No. 41;
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                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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| TOPOLOGY: unknown |
| MOLECULE TYPE: peptide |
| SEQUENCE DESCRIPTION: SEQ ID NO: 54:
| US-10-185-050-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 100.
Lange 6; Conservative
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STATE: New York
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US-10-307-956-17
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Gaps

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We-lo-425-115-359021
Sequence 359021, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: ANOWAILC, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICANION NUMBER: US/10/425,115
CURRENT APPLICANION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
FERRAL 100 SES SEQ ID NOS: 369326
                                                                  RESULT 8
US-10-767-701-31853
US-10-767-701-31853
Sequence 31853, Application US/10767701
Sequence 31853, Application US/10767701
Sequence 31853, Application No. US20040172684A1
Septembral. PROFMARATION:
APPLICANT: Zhou, Yihua
TAPLICANT: Zhou, Yihua
TAPLICANT: Cao, Yongwai
TATLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21/53355 B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 31853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 177;
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US-10-767-701-31853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_90594C.1.pep
US-10-425-115-359021
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 6; Conservative
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  59 TPPPAY 64
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ORGANISM: Zea mays
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Sequence 283015, Application US/10424599

Sequence 283015, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT PILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 283015

LENGTH: 110
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Sequence 48923, Application US/10767701

Sequence 48923, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Chou, Yihua

APPLICANT: APPLICANT: And Wileic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
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                                                                                         Query Match
100.0%; Score 37; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels
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US-10-767-701-48923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_97585C.1.pep
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Best Local Similarity 100.
Matches 6; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-307-956-23
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LENGTH: 132
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P363081C78
CURRENT APPLICATION NUMBER: US/10/245, 859
PRIOR APPLICATION NUMBER: US/059114
PRIOR PILING DATE: 1997-0-17
PRIOR PPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066027
PRIOR PPLICATION NUMBER: 60/06607
PRIOR PPLICATION NUMBER: 60/06607
PRIOR PPLICATION NUMBER: 60/086478
PRIOR PLING DATE: 1998-05-22
PRIOR PPLICATION NUMBER: 60/086478
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-05
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NUMBER OF SEQ ID NOS: 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapien
US-10-245-859-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 TPPPAY 195
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Best Local Similarity
Matches 6; Conserv
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LENGIH: 216
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: FONG, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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PRIOR APPLICATION UNMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 38
LENGTH: 216
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CURRENT APPLICATION NUMBER: US/10/245,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 00/059114
PRIOR PILING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PELING DATE: 1999-10-24
PRIOR PILING DATE: 1999-00-27
PRIOR PELING DATE: 1999-00-22
PRIOR PELING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
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Grimaldi, J. Christopher
Grimely, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Publication No. US20030064474A1
GENERAL INFORMATION:
                                  US-10-245-752-38
; Sequence 38, Application US/10245752
; Publication No. US20030064473A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 6; Conserv
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US-10-245-859-38
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: PS630R1C112
CURRENT PILING DATE: 10502-09-17
PRIOR APPLICATION NUMBER: 10/137942
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 60/063046
                                                     Gaps
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100.0%; Score 37; DB 14; Length 216; larity 100.0%; Pred. No. 4.7e+02; Conservative 0; Mismatches 0; Indels
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Smith, Victoria
Stephan, Jean-Phillippe
Watambe, Colin
Wood, William
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Publication No. US20030068778A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
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Eaton, Dan Filvaroff, Ellen Goddard, Audrey Grimaldi, J. Christopher Gurney, Austin Smith, Victoria Stephan, Jean-Phillippe

APPLICANT: Baker, Kevin APPLICANT: Baton. Dan APPLICANT: Filvaroff Ladre APPLICANT: Goddard, Audre APPLICANT: Grimaldi, J. CAPPLICANT: Smith, Victori APPLICANT: Smith, Victori APPLICANT: Stephan, Jean

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Gaps

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Indels

4.7e+02;

Length 216;

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APPLICANT: Zhang, Zemin
PEPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
; PRIOR FILING DATE: 1998-06-25; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116; SEQ ID NO 38; LENGTH: 216; TYPE: PRT: 7 TYPE: PRT: 7 CRGAMISM: Homo Sapien

US-10-245-107-38
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                                                                                                                                                                                                                                            100.0%; Score 37; DB 14; 100.0%; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT APPLICATION NUMBER: US/10/245,143
CURRENT FILING DATE: 2002-09-16
PRIOR PILING DATE: 2002-09-18
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065014
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/080619
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/080619
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
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Filvarcff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo Sapien
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LENGTH: 216
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                      PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
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APPLICANT: Fong,Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C71
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CURRENT PELING DATE: 2002-09-16
PRIOR PELING DATE: 2002-09-16
PRIOR PELING DATE: 2002-09-16
PRIOR PELING DATE: 2002-07-18
PRIOR PELING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PELING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR PELING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-03
PRIOR PILING DATE: 1998-06-18
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
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Publication No. US20030068779A1
GENERAL INFORMATION:
     FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/065027
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Best Local Similarity 100.
Matches 6; Conservative
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Wood, William
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; ORGANISM: Homo Sapien
US-10-245-103-38
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LENGTH: 216
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Length 216; Indels

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SEQUENCE 38, Application US/10345771

PUBLICART BANKEY, EACH DAIN

APPLICARY: Batch DAIN

APPLICARY: Batch DAIN

APPLICARY: Grimaidi, J. Critatopher

PRIOR PAPLICATION NUMBER: G/050314

PRIOR PAPLICATION NU
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Search completed: October 13, 2005, 14:50:03 Job time : 13.7912 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

October 13, 2005, 14:36:01; Search time 2.50549 Seconds (without alignments) 230.414 Million cell updates/sec

US-09-385-918-16 37 Title: Perfect score:

1 TPPPAY 6 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB Score Result No.

Description	hypothetical prote	•~	transcription acti	probable membrane	probable phage pro	epithelial sodium	hypothetical prote	_		hypothetical prote	EoLF1 protein - hu	BTEB2 protein - hu	hypothetical prote	hypothetical prote	regulatory protein	hypothetical prote	penton protein (II	protein T12A7.2 [i	aconitase XF0290 [	Н	hypothetical prote	_	_	hypothetical prote	_	paired-type homeod	hemoglobin-haptogl	APX-1 protein homo	MAD-3 protein homo
ID	T24298	855019	S68987	D84471	AI0134	I51682	T20528	T41925	T44170	T43984	T09318	S35643	A86521	E72100	A28913	T24856	833938	G88846	G82824	T33486	D84808	T15785	T20096	D71443	T20506	JC7267	B81965	T16213	S71798
90	~	N	N	0	0	N	C3	7	0	~	~	7	~	7	N	7	-	C)	N	7	~	~	~	~	~	~	~	~	0
Match Length	367	455	465	520	556	632	1095	82	88	88	93	219	384	384	432	483	497	520	906	66	214	240	267	274	285	296	357	379	424
Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.9	91.9	91.9	91.9	91.9	91.9	91.9	91.9	91.9	91.9	91.9	91.9	89.2	89.2	89.2	89.3	89.2	89.2	89.5	89.3	89.3	89.2
Score		37				37	37	34	34		34	34	34	34		34	34	34		33	33	33	33	33	33	33	33	33	33
No.	н	7	m	4	ហ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	59

A;Accession: S55019
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: manA
A;Rosidus: 1-455 <SEK>
A;Resaius: 1-455 <SEK>
A;Cross-references: UNIPROT: P42003; EMBL: U10328; NID: G551488; PIDN: AAB60230.1; PID: G55148

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Gaps

. 0

100.0%; Score 37; DB 2; Length 455; ilarity 100.0%; Pred. No. 53; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 6; Conserv

A;Gene: FlyBase:Mad A;Cross-references: FlyBase:FBgn0011648 C;Superfamily: human transcription regulator MAD-4

adenosylmethionine	MAD-2 protein homo	R-SMAD protein, Sm	protein apx-1 [imp	pherophorin-S - Vo	NADH2 dehydrogenas	TonB-dependent rec	ubiquinol oxidase	ba-type ubiguinol	hypothetical prote	armadillo-like pro	envelope glycoprot	endoglucanase C (E	hypothetical prote	epidermal growth f	hypothetical prote
F69904	571797	JE0341	D88991	T10798	T14145	D87331	H87468	B54759	T15230	T03218	T11566	S15271	T23004	A47253	T21432
144 1	167 2	484 2	513 2	599 2	503 2	660 2	665 2	668 2	751 2	766 2	387 2	101 2	227 2	308 2	711 2
89.2	89.2	89.2	89.2	89.2			89.2					89.2	7	89.2	89.2
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Apportence of procession 10128.2 - Caenormabolius elegans
C;Species: Caenormabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24298
B;McMurray, A.
S;McMurray, B.
S;McMurray, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAD polypeptide - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Dacession: S55019
R;Sekelsky, J.J.; Newfeld, S.J.; Raftery, L.A.; Chartoff, E.H.; Gelbart, W.M.
Genetics 139, 1347-1358, 1995
A;File: Genetic characterization and cloning of Mothers against dpp, a gene required for A;Reference number: S55018; MUID;95286061; PMID:7768443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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hypothetical protein T01E8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Cispeciaes: Yersinia peetis
Cispeciaes: All Second Handworth, T. Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F. Nature 413, 523-527, 2001
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Recession: AIQI34
A; Status: preliminary
A; Status: DNA
A; Residues: 1-556 <KUR>
A; Cross-references: UNIPROT:Q8ZH17; GB:AL590842; PIDN:CAC89940.1; PID:g15979164; GSPDB:GR
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis
A;Palmar, S.
A;Palmar, S.
A;Accession: T20528
A;Accession: T20528
A;Accession: T20528
A;Accession: L1095 vMIL.
A;Molecule type: DNA
A;Ross-references: UNIPROT:O19132; EMBL:Z66511; PIDN:CAA91317.1; GSPDB:GN00020; CESP:F0: A;Experimental source: clone F07A11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: alphaxENaC
C;Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I reper
F;355-390/Domain: fibronectin type I repeat homology <1Fl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P51167; EMBL:U23535; NID:g968935; PIDN:AAA74970.1; PID:g96893
C;Genetics:
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                                 probable phage protein YPO1096 [imported] - Yersinia pestis (strain CO92)
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66;
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100.0%; Score 37; DB 2;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-632 <PUO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 37; DB
100.0%; Pred. No. 66;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 6, Conservative
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T20528
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A/Residues: 1-465 <LIU>
A/CRESidues: 1-465 <LIU>
A/CRESidues: 1-465 <LIU>
A/CRESIDUES: 1-465 <LIU>
A/CRESIDUES: 1-465 <LIU>
B/CALDER A/CRESIDUES: WINPROT: 015797; EMBL: US9423; NID: 91438076; PIDN: AAB06852.1; PID: 9143
R/Zhang, Y: Feng, X.H.; Wu, R.Y.; Derynck, R.
Nature 383, 168-172, 1996
A/Title: Receptor-associated Mad homologues synergize as effectors of the TGF-beta respondance number: S71797; MUID: 96311046; PMID: 8774881
A/Accession: S71810
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane transporter [imported] - Arabidopsis thaliana
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
CiAccession: D84471
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                           NyAlternate names: MAD-1 protein; MADR1 protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68987; S71810
R;Liu, F.; Hata, A.; Baker, J.C.; Doody, J.; Carcamo, J.; Harland, R.M.; Massague, Nature 381, 620-623, 1996
A;Title: A human Mad protein acting as a BMP-regulated transcriptional activator.
A;Reference number: S68987; MUID:96238866; PMID:8637600
A;Accession: S68987
A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-465 <ZHA>
C;Superfamily: human transcription regulator MAD-4
C;Keywords: transcription regulation
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C;Superfamily: xanthine permease pbuX
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|TPPPAY 227
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   1 TPPPAY
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Genetics:

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hypothetical protein U24 [imported] - human herpesvirus 6 (strain HST)
C,Species: human herpesvirus 6
A,Variety: strain HST
C,Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C,Accession: T4398
R,Isegawa, Y, Mukan, T, Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawar R, Stsegawa, T, Murol. 73
Y, Murol. 73
Y, Murol. 74
N,Tele: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and IA, Reference number: Z22732; MUID:99412319; PMID:10482554
A,Accession: T43984
A,Accession: T43984
A,Accession: T43984
A,Status: DNA
A,Residues: 1-88 a.ISE>
A,Residues: 1-88 a.ISE>
A,Residues: 1-88 a.ISE>
A,Residues: Legences: UNIPROT:09WT40; EMBL:AB021506; NID:g4995977; PIDN:BAA78245.1; PID:g44
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09J18
R;Nicholas, J.; Martin, M.
J. Virol. 68, 597-610, 1994
A;Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hun
A;Reference number: 216644; MUID:94118404; PMID:8289364
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R;Sogawa, K.; Imataka, H.; Yamasaki, Y.; Kusume, H.; Abe, H.; Fujii-Kuriyama, Y.
Nucleic Acids Res. 21, 1527-1532, 1993
A;Title: CDNA cloning and transcriptional properties of a novel GC box-binding protein, I A;Reference number: S35643; MuID:93241930; PMID:8479902
A;Reference number: S35643
A;Ref
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C;Species: Homo sapiens (man)
C;Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.9%; Score 34; DB 2; Length 88; 83.3%; Pred. No. 30; ive 1; Mismatches 0; Indels
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Pred. No. 32;
1; Mismatches 0; Indels
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A,Molecule type: DNA
A,Residues: 1-93 <NIC>
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83.3%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 5; Conservative
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Best Local Similarity
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TPPPSY 11
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A;Description: Determination and analysis of the complete nucleotide sequence of human h
A;Reference number: 222022
A;Accession: T41925
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <NIC>
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A;Variety: strain 229
A;Variety: strain 229
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000
C;Accession: T44170
R;Dominguez, G.; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
A;Virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human A;Reference number: 222734; MUID:99412318; PMID:10482553
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C;Species: human herpesvirus 7
A;Variety: strain JI
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41925
R;Nicholas, J.
                                                                                                                                                                                                                                                           Gaps
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                                                       A;Map position: 2
A;Introns: 32/2; 202/2; 404/3; 587/3; 794/3; 964/1; 1004/3; 1080/2
                                                                                                                                                                       Query Match
100.0%; Score 37; DB 2; Length 1095;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
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Pred. No. 28;
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A;Residues: 1-88 <DOM>
A;Cross-references: EMBL:AF157706; PIDN:AAD49637.1
A;Experimental source: strain Z29; variant B
A;Note: U24
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83.3%;
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Matches 5; Conservative
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                   A; Gene: CESP: F07A11.4
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Query Match

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RESULT 10

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Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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R;Experimental source: strain CWL029
R;Read, T.D.; Burnham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A;Molecule type: DNA
A;Residues: 1-384 <STO>
A;Cross-references: UNIPROT:Q9JSH3; GB:BA000008; NID:g8978614; PIDN:BAA98451.1; GSPDB:GN
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C;Genetics:
A;Gene: CPn0241; CP0521
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                   hypothetical protein CPj0241 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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Pred. No. 1.4e+02;
1; Mismatches 0; Indels
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Pred. No. 1.4e+02;
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83.3%;
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83.3%;
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Best Local Similarity 83.3%,
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Matches 5; Conservative
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TPPPSY 340
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TPPPSY 340
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A;Residues: 1-384 <ARN>
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A;Gene: CPj0241
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Matches
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RESULT 15

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regulatory protein brlA - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Sate: 30-Jun-1998 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28913
R;Adams, T.H.; Boylan, M.T.; Timberlake, W.E.
Cell 54, 353-362, 1988
A;Title: brlA is necessary and sufficient to direct conidiophore development in Aspergill
A;Reference number: A28913; MUID:88282543; PMID:3293800
A;Title: brlA is necessary and sufficient to direct conidiophore development in Aspergill
A;Residues: 1-432 <ADA>
A;Gross-references: UNIPROT:pl0069
C;Genetics:
C;Genetics: brlA
A;Gene: brlA
C;Keywords: DNA binding; zinc finger
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Pred. No. 1.6e+02;
1; Mismatches 0;
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Job time: 9.5055 secs
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homo sapien mus musculu sapien xenopus lae rattus norv

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P97454 Q9r1v3 Q6i9t1 Q864v7 P79947

Q864V7 P79947

rattus norv sus scrofa brachydanio brachydanio anopheles g

Q6p7a6 Q9i8v2 Q7t082 Q6puc3

SMA1 BRARE 07T082 SMA1 RAT

Last sequence update) Last annotation update)

Created)

37 AA

PRT;

ALIGNMENTS

rattus norv

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[1]—
SEQUENCE FROM N.A.
MEDLINE=22263387; PubMed=12376102; DOI=10.1016/S0012-1606(02)90805-5;
KTATHORE-22263387; PubMed=12376102; DOI=10.1016/S0012-1606(02)90805-5;
Wagner D.S., Achmid B., Imai Y., Talbot W.S., Mullins M.C.,
Hammerschmidt M.;
"Maternally supplied Smad5 is required for ventral specification in zebrafish embryos prior to zygotic Bmp signaling.";
Dev. Biol. 250:263-279(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes;
Cyprinidae, Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BCO16719; AAH16719.1; -. Hypothetical protein.
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100.0%; Pr
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01-DEC-2001 (TrEMBLrel 19,
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
   SEQUENCE FROM N.A.
TISSUE=Bone marrow;
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Best Local Similarity
Matches 6; Conserv
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NCBI_TaxID=9606;
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 0 day neonate lung cDNA. RIKBN [411-length enriched]
11brary, clone:E030041A20 product:hypothetical protein, full insert
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arai K., Kasashima Y., Kuwano A., Yoshihara T.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB106114; BAC66060.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 AA; 10078 MW; 94683F77EF069EA5 CRC64;
                                                                                  4263 MW; B1E82C53C0A7A01E CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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EMBL; AY135144; AAN34935.1; -.
EMBL; AY135143; AAN34935.1; JOINED.
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NON TER 42 42
SEQÜENCE 42 AA; 4263 MW; B1E82C
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Best Local Similarity
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TISSUE=Tendon;
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STRAIN=CS7BL/6J; TISSUE=Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of
60,770 Full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Lung; MEDILINE=20499374; PUBG=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Wuramatsu M., Hayashizaki Y.; Wuramatsu M., Eap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Smad1 (Fragment).
Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
"Functional annotation of a full-length mouse cDNA collection.";
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REGUENCE 116 AA; 12590 MW; E2D2F6B2DA8ED17D CRC64;
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                                  Nature 409:685-690(2001).
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Best Local Similarity 100.
Matches 6; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Lung;
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                                                                  Q81V31
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Q8IV31
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5706 / ATCC 13902 / XV 101;

MEDLINE=2002145; PubMed=12024217; DOI=10.1038/417459a;

Ada Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., Ao Amaral A.M., Bertolinin M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Rais J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Rais J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Ratuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Ratuyama A.M., Madeira A.M.B.N., Martinez-Rossi N.M.,

Mortins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Mortins E.C., Machado M.A., Sena J.A.D., Silva C., de Souza R.F.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

A Trindade dos Santos M., Tuffil D., Teai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                SEQUENCE FROM N.A.
SUDDATE C.J.H., Micol L., McNeilly A.S., Baird D.T.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY035385, AAK61333.1; -.
GO; GO:0006355; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO3165; MH1; 1.
PFam; PF03165; MH1; 1.
  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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100.0%; Pred. No. 1.8e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 37; DB 2; Length 17
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             170 170 170 170 170 AM; 2C1D20CCDBDEE7F3 CRC64;
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1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC2256.
OrderedLocusNames=XAC2256;
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01-OCT-2002 (TrEMBLrel. 22, Created)
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EMBL; AE011862; AAM37109.1; -.
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Best Local Similarity 10v...
6; Conservative
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Best Local Similarity
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                                           NCBI_TaxID=9940;
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36 TPPPAY 41

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MEDINE-2386257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-22386257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
A Klausner R.D., Collins P.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Porshyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,
A Nilalon D.K., Muzny D.M., Sodersia A.M., Gay L.J., Hulyk S.W.,
Yillalon D.K., Muzny D.M., Sodersjene E.J., Lu X., Gibbs R.A.,
A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Schwentz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chul C., Crowley C., Currell B., Douel B., Dowd P., Eaton D., Foster J., Grimmldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Sendien E., Simmons L., Sanch V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieard D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 216 AA; 23729 MW; DFSA7DB1E4126063 CRC64;
                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
5-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotheital protein FLJ90586 (VPMH1932).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. 1.9e+02;
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216 AA
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PRT;
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Genome Res. 13:2265-2270(2003).
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Matches 6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Best Local Similarity 100.
Matches 6; Conservative
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Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                 SEQUENCE FROM N.A.
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                                          NCBI_TaxID=9940;
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SEQUENCE
                         Caprinae;
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EMBL, AK172816; BAD18786.1; - SEQUENCE 216 AA; 23671 MW; DF5A7DB1E411AF63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                        Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Sugaixi Y., Nagai K., Sugano S., Ishii S., Kawai Hio Y., Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AKO75067; BAC11382.1; -- SDSA7DB1E4126076 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBMKC3;
QBONCC3;
QBONCC3. (TERMBLrel. 22, Created)
Q1-OCT-2002 (TERMBLrel. 22, Last sequence update)
Q1-OCT-2003 (TERMBLrel. 25, Last annotation update)
Mand5 (Fragment)
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 37; DB 2; Length 21.
100.0%; Pred. No. 1.9e+02;
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                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ90586.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ23977.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 37; DB 2; L 100.0%; Pred. No. 1.9e+02;
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                                            216 AA
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                                                                                   (TrEMBLrel. 22, Created)
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                                          PRT;
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Best Local Similarity 100...
6; Conservative
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                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                   01-OCT-2002
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                                          Q8NC22
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Q8MKC3
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06 ZME2
1D 06 ZMI
AC 06 ZMI
DT 05 - J
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Turbulne-12236257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Kraushorf R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brapleton M.J., Usdin T.B., Ponaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Hulyk S.W.,

A Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Loquellano A., Young A. C., Shevchenko Y., Boutfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Charles G.J., Marra M.A.,

Charles G. C., March C., Charles C., Schnerch A., Schein J.E.,

Charles G. C., March C., Grimwood J., Schmutz J., Myers R.M.,

Charles G.J., Marra M.A.,

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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05 G0:0005622; C:intracellular; IEA.
GO; G0:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003619; Dwarfin_A.
                                                                                                                                                                                                                              GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001132; Dwarfin.
InterPro; IPR008984; SNAD_FHA.
Pfam; PF03166; MH2; 1.
SWART; SM00524; DWB; 1.
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Souza C.J.H., Baird D.T.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS08027; AAM34248.1; -.
HSSP; Q15797; 1KHU.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment)
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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Gallus.
NCBI_TaxID=9031;
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Q6NW84
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STRAIN-VPI-S482 / ATCC 29148;

MEDLINE-22550858; Pubhed=12663928; DOI=10.1126/science.1080029;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).

EMBL, ABO16391, AAO76298.1; -.

COMDLete protecome.

256 AA; 28486 MW; F4963B890947089D CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
BMP signal transducer Smadl (Fragment).
Gallus gallus (Chicken).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBL_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 37; DB 2; Length 256; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Length 245;
                                                                                                                                                                                                                                                    100.0%; Score 37; DB 2; Length 24
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF233238; AAF36983.1; -.
                                                                                                                                       245 245
245 AA; 27450 MW; 281008651BF043C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BT1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AA.
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Pfam; PF03165; MH1; 1.
SMART; SM0523; DWA; 1.
Hypothetical protein.
NON TER
SEQUENCE 245 AA; 27450
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Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 TPPPAY 6
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овавн6;
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Q919L8
1D Q919L
DT Q019L
DT Q01-OC
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08A8H6
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Gallus gallus (Chicken).
Bukaryota; Metazoa; Chodata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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HSSP; O15797; 1KHU.
TRANSFAG; TO1889; Cintracellular; IEA.
GO; GO:0005622; Cintracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00132; Dwarfin.
InterPro; IPR008694; SwaD_FHĀ.
Pfam; PF03165; MH1; 1.
Pfam; PF03165; MH2; 1.
SWART; SW00523; DWA; 1.
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GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO01132; Dwarfin.
InterPro; IPRO0984; SMAD_FHA.
Pfam; PF03166, MH2; 1.
SMART; SM00524; DWB; 1.
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AFF43239; AAD30150.1; --
HSSP; Q15797; 1KHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 291
291 AA; 32755 MW; 7F9C39B17748E446 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6NW84;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 37; DB 2; L
100.0%; Pred. No. 2.6e+02;
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100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0;
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Best Local Similarity الاست.
الا والا الاستفادة الاست
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Raha S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.W., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2004) to the EWBL/GenBank/DDBJ databases.

L. Submitted (MAR-2004) to the EWBL/GenBank/DDBJ databases.

EMBL; BCG67685; AAH67685.1; -.

R GO; GO: 00006347; C: nucleus; IEA.

R GO; GO: 00006355; P: regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001356; Homeodowa.

R InterPro; IPR001356; Homeodowain like.

R InterPro; IPR001037; Lambda_like_DNA.

R InterPro; IPR001037; POU.

R InterPro; IPR001037; POU.

R Pfam; PF00167; POU: 1...

R Pfam; PF00167; POU: 1...

R Pfam; PF00167; POU: 1...
                                                            TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
PROSITE; PS00035; POU 1; 1.
PROSITE; PS00465; POU 2; 1.
DNA-binding; Homeobox; Hypothetical protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 37; DB 2; Length 334; 100.0%; Pred. No. 38+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AA; 36699 MW; 25031A1FD4FEBD41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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PRINTS; PRO0028; POUDDMAIN.
ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU; 1.
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nes 6; Conservative
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SMART; SM00352; POU; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                       SEQUENCE FROM N.A.
NCBI_TaxID=7955;
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Search completed: October 13, 2005, 15:09:28 Job time : 13.4286 secs

||||||| TPPPAY 26

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1 TPPPAY 6

Best Loca Matches

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Gaps

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October 13, 2005, 14:01:04; Search time 13.5165 Seconds (without alignments) 171.684 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5 US-09-385-918-18 39 1 TPPPGY 6 **BLOSUM62** Perfect score: Scoring table: Sequence: Title:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 ... Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\*
11: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*
8: geneseqp2003bs:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Aab83033 Human Sma	Aab83034 Human Sma	Aab83039 Human Sma	Aab83040 Human Sma	Aaw82838 PY motif	Aaw82837 PY motif	Aaw99363 Human sMA	Aab80934 Human Sma		w	Abp53783 Human Sma	Aaw55965 Amino aci	Aay69623 Human Sma	Aay96726 Human MAD	Aab80935 Xenopus S		Abb08210 Human Sma	Ade34562 Human Mad	Adn95670 Human BEC	Adl61274 Human pro	Human	Adr40443 Human Sma	Ads44736 Bacterial	Aaw18095 Xenopus g	Aaw29459 Mad-relat
	ID	AAB83033	AAB83034	AAB83039	AAB83040	AAW82838	AAW82837	AAW99363	AAB80934	AAW90243	AAB80936	ABP53783	AAW55965	AAY69623	AAY96726	AAB80935	ABP53784	ABB08210	ADE34562	ADN95670	ADL61274	ADP07451	ADR40443	ADS44736	AAW18095	AAW29459
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	Length	9	11	14	14	16	16	381	417	424	424	424	425	425	425	425	425	425	425	425	425	425	425	444	467	467
\$ Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	٠.	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score						39														39					
Result	SO.	1	61	n	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw56692 Mouse tum Aaw56691 Human tum		Aaw90241 Human Sma	Aaw82611 Murine Sm	Aaw82613 Murine Sm	Aaw82610 Murine Sm	Aaw82609 Murine Sm	Aaw82612 Murine Sm	Aaw82595 Mouse Sma	Aaw82608 Murine Sm	Aaw82614 Murine Sm	Aaw82607 Human Sma	Aay85178 Human Sma	Abp53781 Xenopus S	Abp53782 Human Sma	Ade54507 Rat Prote	Ade54505 Human Pro	Ade54501 Human Pro	Ade54503 Rat Prote
AAW56692 AAW56691	AAW90239	AAW90241	AAW82611	AAW82613	AAW82610	AAW82609	AAW82612	AAW82595	AAW82608	AAW82614	AAW82607	AAY85178	ABP53781	ABP53782	ADE54507	ADE54505	ADE54501	ADE54503
22	7 2					7 2	7 2	7 2		7 2		7 3		7 5	7 7		7	7 7
46	467	46	46	467	46	46	46	467	46	46	46	467	467	46	46	467	467	467
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
39	3.9	39		39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
26 27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAB83033 standard; peptide; 6 AA. AAB83033; AAB83033 

Human Smad 2 and Smad 3 PY motif consensus sequence. 25-JUN-2001 (first entry)

Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Somad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif; Smad 2; Smad 3.

Homo sapiens.

WO200116604-A1.

08-MAR-2001.

29-AUG-2000; 2000WO-US023729.

99US-00385918. 30-AUG-1999;

(SIGN-) SIGNAL PHARM INC.

Mercurio FM; Murray BW, Hoekstra MF, Xie W,

WPI; 2001-327913/34.

Screening for modulators of TGF-beta and/or bone morphogenic protein (BMP) mediated signaling useful for treating cancer and osteoporosis by evaluating the ability of agents to modulate Smad protein degradation.

Claim 4; Page 35; 75pp; English.

The present sequence is the Smad PY motif consensus sequence. The PY motif binds to the WW domain of HECT (homologous to E6 carboxyl terminus) as ubsiquitin ligase, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-bets and/or bone morphogenic protein (BMP) mediated signalling of HECT E3 ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular

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levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insufficient TGP-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGP-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif; Smad 2; Smad 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BMP) mediated signaling useful for treating cancer and osteoporosis bevaluating the ability of agents to modulate Smad protein degradation.
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis
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0
                                                                                                                                                                                                                                         100.0%; Score 39; DB 4; Length 6; 100.0%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Smad 2 and Smad 3 PY motif consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercurio FM;
                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 14; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB83034 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ile, Leu
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                                                                                                                                                                                                                                                           Local Similarity 100.
nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-327913/34.
                                                                                                                                                                                                                                                                                                                       1 TPPPGY 6
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TPPPGY
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                                                                                                                                                                                                    Sequence 6 AA;
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                                                                                                                                                                                                                                         Query Match
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HECT E3 ubiquitin ligase activity. The method is useful for stimulating bone formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; HECT; homologous to E6 carboxyl terminus; ubiquitination; HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif.
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                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                            100.0%; Score 39; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB83039 standard; peptide; 14 AA.
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Best Local Similarity 100...
6; Conservative
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                                                                                                                                                                                                                                                                                                                        1 TPPPGY
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                                                                                                                                                                                                       Sequence 11 AA;
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The present sequence is a Smad PY motif. The PY motif binds to the WW domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase, resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The sequence is provided in a specification relating to a method for sequence is provided in a specification relating to a method for sequence is provided in a specification relating to a method for screening for agents that modulate transforming growth factor (TGF)-beta and/or bone morphogenic protein (BMP) mediated signalling. The method for involves evaluating the effect of an agent on binding of HECT E3 ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein HECT E3 ubiquitin ligase activity. The method is useful for stimulating conne formation in a patient or treating a condition associated with insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that inhibit BMP-mediated signalling are useful for treating inflammation, broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer,
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ageing, cancer and infectious diseases. Agents that augment BMP-mediated signalling are useful for stimulating bone anabolism as well as treating broken bones, osteoporosis, and acute or chronic renal failure. Agents that inhibit TGF-mediated signalling are useful for treating cancer, inflammation, neurodegeneration and fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HECT E3 ubiquitin ligase, antiinflammatory; cytostatic; osteopathic; antimicrobial; neuroprotective; transforming growth factor beta; TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling; inflammation; ageing; cancer; infection; bone anabolism; osteoporosis; renal failure; neurodegeneration; fibrosis; PY motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; HECT; homologous to E6 carboxyl terminus; ubiquitination;
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                                                                                                                                                             Length 14;
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Pred. No. 32;
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                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                        1 TPPPGY 6
                                                                                                                                                                                                                                                                   TPPPGY
                                                                                                                      Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding endothelial MAD interactor I - for modulating cell proliferation and differentiation, e.g. in cases of atherosclerosis and cancer of colon or pancreas.
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                      Endothelial MAD interactor protein 1; mothers against dpp; MAD-1; decapentaplegic; human; transforming growth factor-beta; TGF-beta; EMII deficiency; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; atterial inflammation; proliferative disease; cancer; colorectal; pancreatic; antisense; angiogenesis; autoimmune disease; fibrosis; wound healing.
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                                                        4; Length 14;
                                                                                    Indels
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inflammation, neurodegeneration and fibrosis
                                                    DB
32;
                                                                                      Mismatches
                                                        Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                            PY motif of the human MAD-3 protein.
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                                                                                                                                                                                                                     AAW82838 standard; peptide; 16 AA.
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                                                        100.0%;
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                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                             Sequence 14 AA;
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AAW82837;

AAW8283

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New Mothers against dpp (MAD) polypeptide (sMAD3d) and polynucleotide -useful as diagnostic reagents and for prevention and treatment of chronic renal failure, atherosclerosis and fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel Mothers against ddp (MAD) protein encoded by a splice variant, which is required for the signal transduction of DPP (decapentaplegic). The sMAD3d polypeptides and polynucleotides are useful for diagnosing, preventing or treating diseases including chronic renal failure, atherosclerosis and fibrosis
                  Mothers against ddp; MAD; splice variant; signal transduction;
decapentaplegic; diagnosis; renal failure; atherosclerosis; fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smad, Cytostatic; vulnerary, cerebroprotective; immunosuppressive; Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM; Smad Interaction Motif; tissue repair; fibrotic condition; human; immunosuppression; diabetic nephropathy; tumour.
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                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BECKMAN CORP.
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Best Local Similarity
Matches 6; Conserv
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                                                                                Homo sapiens
                                                                                                                                                                                                 22-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding endothelial MAD interactor I - for modulating cell proliferation and differentiation, e.g. in cases of atherosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                    Endothelial MAD interactor protein 1; mothers against dpp; MAD-2; decapentaplegic; human; transforming growth factor-beta; TGF-beta; EMI1 deficiency; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; arterial inflammation; proliferative disease; cancer; colorectal; pancreatic; antisense; angiogenesis; autoimmune disease; fibrosis; wound healing.
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                                                                                                                                                                                             motif of the human MAD-2 protein.
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                                                                            AAW82837 standard; peptide; 16 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US007356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer of colon or pancreas.
                                                                                                                                                        (first entry)
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-583204/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   WO9845467-A1
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Gaps

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Indels

Howell MT;

Hill CS,

Germain SE,

Human sMAD3 splice variant protein.

(first entry)

21-MAY-1999

AAW99363;

BXXXXXX

RESULT 7

AAW99363

Query Match Best Local S: Matches 6

ò g in assays with Smad2, FAST-1 and Smad3, used to develop

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AAB80936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                      The present invention relates to peptides capable of interacting with a Smad protein, comprising a Smad Interaction Motif (SIM, amino acid aced protein, comprising a Smad Interaction Motif (SIM, amino acid are a family of highly conserved, intracellular proteins that signal cellular responses downstream of Transforming Growth Factor-beta (TGF-beta) family serine/threonine kinase receptors. The SIM is thought to be necessary for interaction with the MH2 domain of Smad2. The Smad-interacting peptides of the present invention are useful in the necessary for interaction with the MH2 domain of Smad2. The Smad-interacting peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of manufacture of a medicament for the treatment of a patient in need of reducing extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue formation arising from injury or surgery, or reducing scar tissue formation arising from injury to the brain; a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy crenal disease) or renal fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                         Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of cancer and for tissue remodelling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is less than 32 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transforming growth factor-beta superfamily signalling; modulator; Smad2; TGF-beta; detection; FAST-1; MH2 domain; Smad interaction domain; SID; treatment; developmental; disorder; immunological; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 39; DB 4; Length 41
100.0%; Pred. No. 5.8e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW90243 standard; protein; 424 AA
                                                                                                                                                                                                        Claim 6; Fig 12; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US010983
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Best Local Similarity 100...
G; Conservative
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WPI; 2001-265836/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 TPPPGY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TPPPGY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 417 AA;
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ò g Modulating TGF-beta superfamily signalling - comprises use of compounds

(HARD ) HARVARD COLLEGE.

WPI; 1999-059773/05.

N-PSDB; AAV72113

Whitman M, Chen X;

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                                                                               This sequence represents a human Smad3 protein which is used in a method to detect a compound capable of modulating transforming growth factor-bata feater family signalling. The invention describes a complex which forms between FAST-1 and Smad2 and this complex is specifically induced by signals generated by a TGF-beta superfamily member. A domain of FAST-1 directly interacts with Smad2 and this interaction is mediated by specific domains of the two interaction gonelecules, manaly, the MH2 domain of Smad2 and the Smad interaction domain (SID) of FAST-1. The methods and compounds described are useful for the detection and treatment of conditions involving abnormal TGF-beta superfamily signalling. They can be used to treat e.g. developmental disorders, immunological disorders and cancer. The products can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to peptides capable of interacting with a Smad protein, comprising a Smad Interaction Motif (SIM; amino acid sequence PP(T/N) X). The present sequence is a Smad protein. Smad proteins are a family of highly conserved, intracellular proteins that signal cellular responses downstream of Transforming Growth Factor-beta (TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptide capable of interacting with a Smad polypeptide, useful in the treatment of cancer and for tissue remodalling or healing of a wound, injury or surgery, comprises a Smad Interaction Motif and is less than 32 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smad, Cytostatic, vulnerary, cerebroprotective, immunosuppressive, Anti-HIV; antidiabetic; ophthalmological; antiinflammatory; SIM; Smad Interaction Motif; tissue repair; fibrotic condition; human; immunosuppression; diabetic nephropathy; tumour.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 424;
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products for treating, e.g. developmental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 39; DB 2; I
100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
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                                            Example XII; Page 60-61; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80936 standard; protein; 424 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Fig 12; 179pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-265836/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Smad3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 TPPPGY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TPPPGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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beta) family serine/threonine kinase receptors. The SIM is thought to be necessary for interaction with the MHZ domain of Sma2. The Smadinteraction peptides of the present invention are useful in the manufacture of a medicament for the treatment of a patient in need of cately of a medicament for the treatment of a patient in need of reducing extracellular matrix deposition, encouraging tissue repair and/or regeneration, tissue remodelling or healing of a wound, injury or bring a patient with or at risk of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states associated with immunosuppression (such as different forms of malignancy, or injury diseases, and AIDS), diabetic nephropathy, tumour growth, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy or non-inflammatory renal disease) or renal fibrosis
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Seguence 424 AA;

Gaps ö 100.0%; Score 39; DB 4; Length 424; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels Ouery Match Best Local Similarity الاست الاست 1 TPPPGY 6 a

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178 TPPPGY 183

RESULT 11

ABP53783 standard; protein; 424 AA.

ABP53783;

(first entry) 06-JAN-2003 Human Smad3 (HSmad3) protein sequence.

Smad; Smad interacting protein; XFast-3; Antennapedia helix 3; FAST; activin response factor; ARF; cytostatic; vulnerary; antidiabetic; anti-HIV; nephrotropic; activin; transforming growth factor beta; TGF-beta; signalling; cancer; tissue repair; immunosuppression; malignancy; chronic degenerative disease; AIDS; diabetic nephropathy; tumour growth, kidney damage; obstructive nephropathy; immunoglobulin A nephropathy; IgA nephropathy; renal disease.

Homo sapiens.

WO200270702-A2 12-SEP-2002. 28-FEB-2002; 2002WO-GB000877.

01-MAR-2001; 2001GB-00005063.

(IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.

Howell M; Randall R, Hill C,

WPI; 2002-732794/79.

New interacting polypeptide capable of interacting with an activin response factor component, useful in medicine or for the manufacture of a medicament for treating diabetic nephropathy, tumor growth, kidney damage wound healing.

Disclosure; Fig 3; 153pp; English.

The present invention describes a polypeptide (I) capable of interacting (i.e. interacting polypeptide) with an activin response factor (ARF) component. The interacting polypeptide comprises: (a) a Fast motif 1 (FM1) and/or a Fast motif 2 (FM2), and is less than 84, 83, 82, 81, 75, 70, 65, 60, 55, 50, 45, 40, 35, 31, or 30 amino acids in length; ABP53783

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 ABP5

XX
 AB

CC (b) the amino acid sequence LPTSY (S1) and/or PNXXXP(P/L) (S2) or C (S) (6, 6, 55, 80, 45, 40, 40, 35, 32, 31, or 30 amino acids in length; or (c) a (E, 60, 55, 80, 45, 40, 40, 35, 32, 31, or 30 amino acids in length; or (c) a (EM1 and/or FM2 motif, e.g. the sequence of S1, or 3 or 4 out of 5 of its residues, and is not full-length Xenopus, CC residues, or out of 5 of its residues, and is not full-length Xenopus, CC zebrafish or human FAST1 or its fragment, mouse FAST2 or Xenopus FAST3.

CZ EDATAGISH OF VULDERARY, anti-HIV, antidiabetic and nephrotropic activities. (I) can have a transforming growth factor (TGF) agonist beta, activin agonist or activit antagonist mechanism of activities. (I) can have a transforming growth factor (TGF) agonist beta, activit amedicine or in the manufacture of a ction. (I) can be used in a medicine or in the manufacture of a ction. (I) can be used in a medicine or in the manufacture of a ction of activity member signalling; (ii) with cancer; (iii) cropair and/or regeneration, issue remodeling or healing of a wound, in need of reducing extracellular matrix deposition, encouraging tissue cropair and/or regeneration, issue remodeling or healing of a wound, injury or surgery, or reducing scar tissue formation arising from injury to the brain; or (iv) with or at risk of end-stage organ failure, condition, disease states associated with immunosuppression (e.g. different forms of mangue (e.g. obstructive nephropathy, immunoglobulin A (IgA) nephropathy or non-inflammatory renal disease) or renal fibrosis. The present sequence represents a human smad3 (HSmad3) creal fibrosis. The exemplification of the present invention 

Sequence 424 AA;

Gaps .. 0 Length 424; 0; Indels 100.0%; Score 39; DB 5; I 100.0%; Pred. No. 5.9e+02; iive 0; Mismatches 0; Ouery Match Best Local Similarity الاس. الاستراكية في المتراكية في ال

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TPPPGY 183 φ 1 TPPPGY ò 요

RESULT 12

AAW55965 standard; protein; 425 AA. AAW55965

AAW55965;

17-AUG-1998 (first entry)

Amino acid sequence of human MADr3 protein.

Human; MAD; Mothers against DPP; Drosophila decapentaplegic; MADr3; transforming growth factor-beta; TGF-beta; signal transduction; BMP2; BMP4; MADr4; wound healing; AIDS dementia; treatment; ocular disorder; kidney; liver; prevention; scarring; ulcer; corneal incision; cancer; renal failure; arthritis; osteoporosis; atherosclerosis; polycystic kidney disease; congestive heart failure. 

Ношо

EP837073-A1.

22-APR-1998

97EP-00308160. 15-OCT-1997; 96US-00732028. 16-OCT-1996; (SMIK ) SMITHKLINE BEECHAM CORP.

Laping NJ;

WPI; 1998-219071/20. N-PSDB; AAV26065. DNA encoding human MAD protein - useful for producing recombinant protein, gene therapy, etc.

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AAY96726;
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                            Matches
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                          The present sequence represents a human MAD (Mothers against DPP (Drosophila decapentaplegic) (sic)) homologue, designated MADr3. Different transforming growth factor-beta (TGF-beta) family members may signal through different MAD isoforms. MAD proteins have been found to be required for signal transduction of DPP and BMP2/BMP4. MADr3 and MADr4 polypeptides can be used to stimulate wound healing, to restore normal neurological function after trauma or AIDS dementia, to treat ocular disorders, to target certain cells, to treat kidney and liver disorders, to prevent scarring, to treat ulcers and corneal incisions or to treat cancer. MADr3 antagonists can be used to treat renal failure, wound healing and prevention of scar formation, arthritis, osteoporosis, atherosclerosis, polycystic kidney disease and congestive heart failure. The polypeptides can be used to detect and diagnose disease
                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents human Smad3. The Smad proteins are a family of cytosolic proteins which are involved in TGF-beta superfamily signal transduction. On ligand binding, TGF-beta superfamily proteins (Such as bone morphogenetic protein (BMP), activin and TGF-betas themselves) phosphorylate Smad proteins, which then homo- or heterodimerise and translocate to the nucleus to activate target gene transcription. Smad3 (also known as MADB3, hMAD3 and JV15-2) is a member of a subgroup of Smad family transcription factors, the pathway- restricted Smads, which are regulated by TGF-beta and activins. It can heterodimerise with Smad4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense inhibition of the human Smad3 gene, useful for diagnosing, preventing and treating conditions associated with Smad3 expression e.g.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smad3; MADH3; hMAD3; JV15-2; TGF-beta signalling pathway;
transcription factor; expression inhibition; antisense therapy;
tumour formation; inflammation.
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                                                                                                                                                                                                                                                                                          Length 425;
                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                       100.0%; Score 39; DB 2; I 100.0%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                        Mismatches
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5; Fig 1; 47pp; English.
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                                                                                                                                                                                                                                                                                                                          6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             179 TPPPGY 184
                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                          Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                        1 TPPPGY
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                                                                                                                                                                                                                                                                                       Query Match
Claim
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AA469623
ID AAY69623
XX AAX69
XX AAX69
DT 19-AP
XX Smad3
XW trans
XX COC 11-JA
XX COC TAIS
XX AAL18
PT DR WPI;
DR WPSD
XX AAL18
CC TAIS
CC TAIS
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(US6013787-A, AAV69622), the complex being able to activate TGF-beta inducible transcription. The invention relates to antisense objognucleotides targetted to the human Smad3 gene, which inhibit its expression. A series of oligonucleotides (AAZ5796-Z59735) were designed to target different regions of the human Smad3 RNA, and were analysed for their effect on Smad3 mRNA levels by quantitative real-time PCR. The oligonucleotides of the invention are useful for diagnosis, prevention and treatment of conditions associated with Smad3 expression, such as tumour formation, inflammation and certain infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The C-terminal 20 amino acids of this novel MADr3 polypeptide is an inhibitor (antagonist) of ALKS, a receptor involved in the transforming growth factor-beta (TGF-beta) signalling pathway. ALKS inhibitors can be used to treating diseases and conditions in mammals associated with TGF-beta. MAD (Mothers against DPP) is necessary for signal transduction of DPP (brosophila MAD ALKS inhibitors are useful to treat chronic renal disease, acute renal disease, wound healing, arthritis, osteoporosis, thinky disease, uncertaintend neurological function, ocular disorders, trophic conditions, ulcers, Alzheimer's disease, atherosclerosis, restenosis, diabetic neuropathy and any disease where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating diseases and conditions associated with the human protein MADr3 e.g. atherosclerosis, renal disease and Alzheimer's disease comprises administration of an inhibitor of ALK5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MADr3; decapentaplegic; DPP; MAD; Mothers against DPP; vulnerary; transforming growth factor beta; TGF-beta; anti-arthritic; osteopathic; nephrotropic; cardiant; opthalmological; nootropic; neuroprotective; anti-arteriosclerotic; vasotropic; anti-arteriosclerotic; vasotropic; anti-diabetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 39; DB 3; I
100.0%; Pred. No. 5.9e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96726 standard; protein; 425 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fibrosis is a major component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US029924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human MADr3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442272/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 425 AA;
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Gaps

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Indels

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Mismatches

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The present invention relates to peptides capable of interacting with a Smad protein, comprising a Smad Interaction Motif (SIM; amino acid sequence PP(T/N)K). The present sequence is a Smad protein. Smad proteins care a family of highly conserved, intracellular proteins that signal callular responses downstream of Transforming Growth Factor-beta (TGF-Colullar responses downstream of Transforming Growth Factor-beta (TGF-Colullar responses downstream of Transforming Growth Factor-beta (TGF-Colullar responses downstream of Intracellular present in the MH2 domain of Smad2. The Smad-Columpacture of a medicament for the treatment of a patient in need of manufacture of a medicament for the treatment of a patient in need of columpacture of activin or TGF-beta signalling; cancer; a patient in need of and/or regeneration, tissue remodelling or healing of a wound, injury or columpacture actually some formation arising from injury or the trains of end-stage organ failure, pathologic extracellular matrix accumulation, a fibrotic condition, disease states of associated with immunosuppression (such as different forms of malignancy, chronic degenerative diseases, and AIDS), diabetic nephropathy, tumour convent, kidney damage (for e.g. obstructive neuropathy, IgA nephropathy, con non-inflammatory renal disease) or renal fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smad; Cytostatic; vulnerary; cerebroprotective; immunosuppressive; Antidiabelt; ophthalmological; antiinflammatory; SIM; Smad Interaction Motil; tissue repair; fibrotic condition; immunosuppression; diabetic nephropathy; tumour.
Query Match 100.0%; Score 39; DB 3; Length 425; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB80935 standard; protein; 425 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Germain SE, Hill CS,
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N-PSDB; AAF81388.
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                                                                                                                                                             1 TPPPGY 6
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AAB800935 II
AAB80093
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100.0%; Score 39; DB 4; Length 425; 100.0%; Pred. No. 5.9e+02;

Query Match Best Local Similarity

Sequence 425 AA;

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completed: October 13, 2005, 15:00:38
ne : 15.5165 secs
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6; Conservative
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amino acid
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Best Local Similarity
Matches 6; Conserv
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TPPPGY 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 42,
Sequence 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8,
Sequence 2,
Sequence 8,
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Sequence 2,
Sequence 3,
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                                                                                                                                                                                                                                                                                                                                                                                          Description
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('Ggn2_6/ptodata1/iaa/5A_COMB.pep:*

('Ggn2_6/ptodata1/iaa/5B_COMB.pep:*

('Ggn2_6/ptodata1/iaa/6A_COMB.pep:*

('Ggn2_6/ptodata1/iaa/6A_COMB.pep:*

('Ggn2_6/ptodata1/iaa/BECOMB.pep:*

('Ggn2_6/ptodata1/iaa/PCTUS_COMB.pep:*

('Ggn2_6/ptodata1/iaa/backfiles1.pep:*
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-732-028-2
US-09-096-7768-8
US-09-923-922-8
US-09-949-016-6670
US-08-840-76-6
US-08-840-76-6
US-08-701-582D-4
US-08-701-582D-4
US-08-701-582D-4
US-09-082-039A-15
US-08-840-76-42
US-08-840-76-42
US-09-086-7768-7
US-09-087-134-2
US-09-552-138-2
US-09-552-138-15
US-08-552-138-15
US-08-552-138-15
US-09-552-138-15
US-09-923-922-7
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                                                                                                                         513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                          protein search, using sw model
                                                                                                                                       Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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                                                                                                              1 TPPPGY 6
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Perfect score:
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Maximum DB
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                                                                                                                                                          Searched:
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28 39 100.0 488 4 48.50-940-67-533 Sequence 563. Appl 210.0 719 4 18.50-940-717-55 Sequence 51. Appl 210.0 719 4 18.50-947-117-55 Sequence 51. Appl 210.0 719 4 19.50-9471-1166-12 Sequence 51. Appl 210.0 710-12 Sequence 51. Appl 210.0 719 4 19.50-9471-1166-12 Sequence 51. Appl 210.0 719 4 19.50-9471-1166-12 Sequence 51. Appl 210.0 710-12 Seq
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ATTORNEY/AGENT INFORMATION:
NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE/DOCKET NUMBER: SBC ATG 50030
TELECOMMINICATION:
TELEPHONE: 610-270-5015
                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 424 amino acids TYPE: amino acidd STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
CURRENT APPLICATION DATA
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                                                Sequence 14, Application US/08844312
Patent No. 5948639
CENERAL INFORMATION:
APPLICANT: Carlos J. Gimeno and Dean A. Falb
TITLE OF INVENTION: No. 5948639e1 TGF-{SYMBOL 98 \f "Symbol"} Pathway Genes
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD, LLP
STREET: 60 State Street, Suite 510
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                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,312
FILING DATE:
CLASSITCATION A 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MI-013
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 02110
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTIONE
COMPUTER: IBM COMPACTIONE
SOFTWARE: FASESEQ FOR Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 6; Conservative
                                                                                                                                                                                                                      CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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7 TPPPGY 12
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                                  US-08-844-312-14
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Gaps
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US-08-732-028-2
Factor C 2, Application US/08732028
Factor No. 5866633
Factor No. 5866633
Factor No. 5866633
Factor No. 5866634
Factor No. 5866683
Factor No. 586687208
Factor No. 586687208
Factor No. 586088728
Factor No. 586088738
Factor No. 586088728

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100.0%; Score 39; DB 3; Length 424;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,028
FILING DATE:
CLASSIFICATION: 514
APPLICATION NUMBER: US/09/087,134
FILING DATE: 27-MAY-1998
CLASSIFICATION
PULASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,991
FILING DATE: 28-MAY-1997
ATTORNEY AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 00246/501002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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COTHER INFORMATION: Human Smad3
US-09-087-134-8
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, APPLICANT: VENTER, J. Craig et al.
, TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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APPLICANT: MIYAZONO, KOhei
APPLICANT: MIYAZONO, KOhei
APPLICANT: MIYAZONO, KOhei
TITLE OF INVENTION: SMAD6 AND USES THEREOF
FILE REFERENCE: L0461/7120
CURRENT APPLICATION NUMBER: US/09/923,922
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/049,990
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/049,990
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-07-18
PRIOR APPLICATION NUMBER: US 60/066,173
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NOS: 10
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; Patent No. 6812339
                                             08/732,028
                                                                                              NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REPERROCE/DOCKET NUMBER: ATG-
TELECOMMUNICATION INFORMATION:
TELERAX: 610-407-0700
TELERAX: 610-407-0700
TELERAX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-923-922-8; Sequence 8, Application US/09923922; Patent No. 6534476
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  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 16-0CT-1996
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100...
6; Conservative
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MOLECULE TYPE: protein

US-09-183-228-2
                                                                                                                                                                                                                                                                                                                        single
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US-09-923-922-8
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Best Local Similarity
6; Conserve
                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAPING, NICHOLAS J.
APPLICANT: LAPING, NICHOLAS J.
TITLE OF INVENTION: HUMAN MAD PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: RATHER & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Miyazono, Kohei
APPLICANT: Mayazono, Kohei
APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAD6 AND USES THEREOF
FILE REFERENCE: L0461/7038
CURRENT APPLICATION NUMBER: US/09/096,7768
CURRENT FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/049,990
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-07-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPBRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,228
FILING DATE: 30-OCT-1998
                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-096-776B-8
; Sequence 8, Application US/09096776B
Parent No. 6270994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09183228
Patent No. 6309856
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-732-028-2
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                                                                                                                                                                                Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 TPPPGY 184
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Best Local Similarity
Matches 6; Conserv
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US-09-183-228-2
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 836-667
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 amino acids
                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                               205 TPPPGY 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                             US-09-949-016-7630
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-701-582D-2
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US-08-701-582D-4
                                                                                                                                 LENGTH: 451
TYPE: PRT
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-09
NUMBER: 06/237,768
PRIOR PILING DATE: 2000-09-09
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6670
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Batent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Ringler, Kenneth W.
APPLICANT: Ringler, Gregory J.
APPLICANT: Ringlar, Sam
ITILE OF INVENTION: MAD-Related Genes in the Human; FILE REPERCE: 01107.05548
CURRENT APPLICATION NUMBER: US/08/840,767B
CURRENT FILING DATE: 1997-04-16
EARLIER PEPLICATION NUMBER: 60/015,823
ERRIER PILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-08-840-767-6
Fequence 6, Application US/08840767B
; Parent No. 6255464
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
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CRGANISM: Homo sapiens
US-08-840-767-6
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-949-016-7630
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100.0%; Score 39; DB 4; Length 451; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                               Sequence 2, Application US/08701582D
Fatent No. 6017755
GENERAL INFORMATION:
FAPLICANT: WRANN, Jeffrey
APPLICANT: ATTISANO, Liliana
APPLICANT: STEEPHEN W.
TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: Virginia
CONTRY: U.S.A.
ZIP: 2213-1404
ZOBPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BACHOLIN Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,582D
FILING DATE: 22-AGG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanek
REGISTRATION NUMBER: 024916-004
TELECOMMUNICATION INFORMATION:
MATERIAL OF MEDIUM INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Tamaki, Kiyoshi
APPLICANT: Wernstedt, Christer
APPLICANT: Piek, Esther
APPLICANT: Piek, Esther
APPLICANT: Piek, Esther
APPLICANT: Piek, Esther
APPLICANT: Piek, Bather
APPLICANT: Fiek, Peter
APPLICANT: Weldin, Carl-Henrik
TITLE OF INVENTION: WATH SMAD2
NUMBER OF ESQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 39; DB 3; Length 467; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: TBM Compatible
COMPUTER: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,039A
FTLING DATE: 20-MAY-1998
FTLING DATE: 214
                                           OPERATING SYSTEM: DOS CONTROLLS OF PERATING SYSTEM: DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: 60/047,807 FILING DATE: 20-MAY-1997 PRIOR APPLICATION NUMBER: 60/081,313 ATTORNEY/AGENT INFORMATION: NAME: JOHN R. Van Amsterdam REGISTRATION NUMBER: L0461/7036 TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: 617-720-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Patent No. 6103669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
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US-09-082-039A-15
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APPLICANT: Souchelnytskyi, Serheyi
APPLICANT: Tamaki, Kiyoshi
APPLICANT: Tamaki, Kiyoshi
APPLICANT: Tamaki, Kiyoshi
APPLICANT: Wernstedt, Christer
APPLICANT: Wernstedt, Christer
APPLICANT: Piek, Esther
APPLICANT: Piek, Bether
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: SMAD2 PHOSPHORYLATION AND INTERACTION
TITLE OF INVENTION: WITH SMAD4
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 39; DB 3; Length 467; 100.0%; Pred. No. 1e+02; ive 0; Mismatches 0; Indels
| Sequence 4, Application US/08701582D |
| Patent No. 6017755 |
| GENERAL INFORMATION: APPLICANT: WRANA, Jeffrey |
| APPLICANT: WTANA, Jeffrey |
| APPLICANT: ATTISANO, Liliana |
| TITLE OF INVENTION: MADR2 TUMOUR SUPPRESSOR GENE |
| TUMBER OF SEQUENCES: 24 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Burns, Doane, Swecker & Mathis |
| STREET: PO. Box 1404 |
| CITY: Alexandria |
| STATE: Virginia |
| COUNTRY: U.S.A. |
| COUNTRY: U
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,582D
FILING DATE: 22-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REA, Teresa Stanck
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 024916-004
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-620
TELEFAN: (703) 836-620
TELEPAN: (703) 836-630
TELEPAN: (703) 836-630
TELEPAN: (703) 836-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-1404
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6103869
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Best Local Similarity 100.
Matches 6; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: MA
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US-09-082-039A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-WAY-1997
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 60/081,313
FILING DATE: 10-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: John R. Van Amsterdam
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-350
TELEFAX: 1017-20-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-08-840-767-42
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220 TPPPGY 225
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US-08-840-767-42
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Search completed: October 13, 2005, 14:03:08 Job time : 3.98214 secs

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Sequence 19, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 343464,
Sequence 43198, A
Sequence 353466,
Sequence 296400,
Sequence 296400,
                                              ; Search time 12.7912 Seconds (without alignments)
195.471 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-307-956-19
US-10-307-956-24
US-10-307-956-25
US-10-425-115-344905
US-10-425-115-353466
US-10-425-115-353466
US-10-767-701-34928
US-10-767-701-34928
US-10-425-115-353469
                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                       1859788 seqs, 416717961 residues
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                                               October 13, 2005, 13:59:34;
                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
                                                                                                                        Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                              US-09-385-918-18
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Maximum DB
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Sequence 353473, Sequence 62416, A Sequence 70132, A Sequence 31883, Sequence 295775, Sequence 2, Appli Sequence 2, Appli Sequence 46, Appli Sequence 16, Appli Sequence 17, Appli Sequence 7, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 2, Appli Sequence 253413, Appli 25413, Appli 25413
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51, Appl
333129,
295770,
333133,
108833,
1639, Ap
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242437,
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Sequence 33.
Sequence 29
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ALIGNMENTS
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Sequence 18, Application US/10307956
| Publication No. US20030119072A1
| GENERAL INFORMATION:
| APPLICANT: Hockstra, Merl F. |
| APPLICANT: Murray, Brion |
| APPLICANT: Marcurio, Frank |
| TITLE OF INVENTION: MRANDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS |
| TITLE OF INVENTION: MUMBER: US/10/307,956 |
| CURRENT APPLICATION NUMBER: US/10/307,956 |
| CURRENT FILING DATE: 2002-12-02 |
| PRIOR APPLICATION NUMBER: US/09/385,918 |
| PRIOR FILING DATE: 1999-08-30 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 18
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llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
Matches 6; Conserv
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RESULT

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Sequence 19, Application US/10307956
; Publication No. US20030119072A1
; General Information:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xie, Wellin
APPLICANT: Murray, Brion
APPLICANT: Murray, Brion
APPLICANT: Merray, Brion
APPLICANT: Merray, Brion
APPLICANT: Merray, Brion
FILE REFERENCE: 860098-433
CURRENT APPLICATION NUMBER: US/10/307,956
CURRENT FILING DATE: 2002-12-02
FRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENTH: 11
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; Publication No. US20030119072A1
; General Information:
    General Information:
    General Information:
    APPLICANT: New Heal in
    APPLICANT: Murray, Brion
    APPLICANT: Murray, Brion
    APPLICANT: Merray, Brion
    TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
    FILE REFERENCE: 860099.433
    CURRENT APPLICATION NUMBER: US/10/307,956
    CURRENT FILING DATE: 1999-08-30
    NUMBER OF SEQ ID NOS: 32
    SEOFFWARE: PastSEQ for Windows Version 3.0
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COTHER INFORMATION: Xaa = Isoleucine or Leucine US-10-307-956-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 14
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RESULT 4 US-10-307-956-25 ; Sequence 25, Application US/10307956 ; Publication No. US20030119072A1

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APPLICANT: Murray, Brion
APPLICANT: Marray, Brion
APPLICANT: Mercurio, Frank
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
TITLE OF INVENTION: MUMBER: US/10/307,956
CURRENT APPLICATION NUMBER: US/09/385,918
PRIOR APPLICATION NUMBER: US/09/385,918
PRIOR FILING DATE: 1999-08-30
PRIOR SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PRIOR PRIOR PRIOR FILING DATE: US/09/385,918
TYPEE: REACHEN SM: US/09/385,918
TYPEE: REACHEN SM: US/09/385,918
US-10-307-956-25
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APPLICANT: La Rovaic, David K.
APPLICANT: APPLICANT: Cao, Yinua
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yinuai
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)8
FULE REPERENCE: 28-21(5322)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 344905
LENGTH: 65
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US-10-425-115-344905
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(65)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 353464, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 344905, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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APPLICANT: Hoekstra, Merl F. APPLICANT: Xie, Weilin
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Best Local Similarity luv...
6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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    ORGANISM: Zea mays
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US-10-767-701-34928
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US-10-767-701-43198

Sequence 43198, Application US/10767701

Sequence 43198, Application No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(5355)8

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 43198

LENGTH: 78
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Covalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cano, Yongue
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-2153222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 353464
LENGTH: 72
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                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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US-10-767-701-43198
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100.0%; Score 39; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_85534C.1.pep
US-10-425-115-353464
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Best Local Similarity 100.
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ORGANISM: Sorghum bicolor
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63 TPPPGY 68
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LENGTH: 116
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US-10-425-115-296400

US-10-425-115-296400

SQUENCE 296400, Application US/10425115

SQUENCE 296400, Application US/10425115

SQUENCE 296400, Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
FILE REFERENCE: 30-21 (53222)
CURRENT APLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 296400

LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                    Sequence 34928, Application US/10767701

Sequence 34928, Application US/10767701

GENERAL INFORMATION:
GENERAL INFORMATION:
The OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 118

LENGTH: 118
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US-10-767-701-34928
                                                                                               100.0%; Score 39; DB 16;
100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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US-10-425-115-296400
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85536C.1.pep
US-10-425-115-353466
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Sequence 353473, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION: Thomas J. APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
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54 TPPPGY 59
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                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
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US-10-425-115-242437
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Sequence 314821, Application US/10425115
Publication No. US20040214272A1
Sequence 314821, Application US/10425115
Sequence 314821, Application No. US20040214272A1
SELECATE TOWNERTION: David K.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 314821
LENGTH: 158
                                                                                      US-10-425-115-353469

Sequence 353469, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)
FURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/426

CURRENT SEQ ID NOS: 369326

SEQ ID NO 353469
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 2.4e+02;
cive 0; Mismatches 0;
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; OTHER INFORMATION: Clone ID: MRT4577_85539C.1.pep
US-10-425-115-353469
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OTHER INFORMATION: Clone ID: MRT4577_50179C.1.pep
US-10-425-115-314821
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US-10-425-115-333728
; Sequence 333728, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 6, Conservative
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Best Local Similarity 100.
6, Conservative
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123 TPPPGY 128
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34 TPPPGY 39
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| TPPPGY 59
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ORGANISM: Zea mays
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Thous Yilua
APPLICANT: Cao, Yingwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333728
LENGTH: 208
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Sequence 242437, Application US/10425115
Publication No. US2004021427241
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100.0%; Score 39; DB 16; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 39; DB 16; Length 208; 100.0%; Pred. No. 3.1e+02;
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// OTHER INFORMATION: Clone ID: MRT4577_152689C.1.pep
US-10-425-115-242437

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US-10-425-115-333728
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LOCATION: (1)...(208)
OOTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(227)
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FEATURE:
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## APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwel

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NOS: 369326

BENTH: 302

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_85542C.1.pep
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293 TPPPGY 298
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Search completed: October 13, 2005, 14:50:03 Job time : 12.7912 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

October 13, 2005, 14:36:01; Search time 2.50549 Seconds (without alignments) 230.414 Million cell updates/sec

US-09-385-918-18 Perfect score: Title:

1 TPPPGY 6 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# STIMMARTES

ES	Description	hypothetical prote	MAD-3 protein homo	adenosylmethionine	MAD-2 protein homo	R-SMAD protein, Sm	Ϊ,	endoglucanase C (E	hypothetical prote	Ψ	hypothetical prote	_	v	bic	arginine decarboxy	ß	>-	probable membrane	_	_	hypothetical prote			prot	class I	unknown protein, 5	hypothetical prote	_	cal	nrobable ABC trans
SUMMARIES	ΩI	D71443	S71798	F69904	S71797	JE0341	T10798	S15271	T21432	833621	T14313	S71558	T30764	AD1863	T15046	T12525	A57541	852507	S18529	T46900	C87544	S09804	F72506	E86261	S14981	D96663	G70578	AB2080	ശ	G95887
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	Score							39										34	34	34	34	34	34	34	34	34	34	34	34	34
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hypothetical prote	branched-chain-ami	branched-chain ami	probable membrane	hypothetical prote	hypothetical prote	hypothetical prote	CCAAT/enhancer bin	CCAAT/enhancer-bin	poly(beta-d-mannur	hypothetical prote	poly(beta-D-mannur	hypothetical prote	hypothetical prote	CCAAT/enhancer bin	hypothetical prote
G84494	A34082	AD0924	T36845	T34525	D70728	T33421	JC4311	A54265	H83202	T32730	JN0777	T48052	T49578	I49575	AD1808
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291	308	309	319	319	325	344	358	358	367	367	368	380	393	395	399
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1
D71443
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: D71443
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 Nature 391, 485-488, 1998
 A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
 C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A. Do. Economic Animbox. A71400. MITD. 00171113. DMTD. 0461716

A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: D71443
A;Accession: D71443
A;Accession: D71443
A;Molecule type: DNA
A;Residues: 1-274 <BEV>A;Residues: 1-274 <BEV>A;Cross-references: UNIPROT:023583; GB:Z97343; NID:g2245073; PID:e327059; PID:g2245099
C;Genetics:
A;Map position: 4COP9-4G3845

Gaps o. Query Match 100.0%; Score 39; DB 2; Length 274; Best Local Similarity 100.0%; Pred. No. 25; Matches 6; Conservative 0; Mismatches 0; Indels

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|||||| 196 TPPPGY 201 1 TPPPGY 6 ò g

RESULT 2

MAD-3 protein homolog - human C;Species Homo sapiens (man) C;Species Homo sapiens (man) C;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 02-Sep-2000 C;Accession: S71798 K;Zhang, X. H; Wu, R.Y.; Derynck, R. Nature 383, 168-172, 1996 A;Title: Receptor-associated Mad homologues synergize as effectors of the TGF-beta respo A;Title: Receptor-associated Mad homologues synergize as effectors of the TGF-beta respo A;Reference number: S71797; MUID:96371046; PMID:8774881 A;Accession: S71798 A;Accession: preliminary; nucleic acid sequence not shown

A;Residues: 1-424 <ZHA> A;Cross-references: EMBL:U68019 C;Superfamily: human transcription regulator MAD-4

Length 424; DB 2; 39; Score 39; Pred. No. 100.0%; Query Match Best Local Similarity N

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6; Conservative

Matches

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178 TPPPGY 183

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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-484 <DAH>
A,Cross-references: UNIPROT: Q9TZQ2; GB: AF078529; NID: g3978423; PIDN: AAC83344.1; PID: g397
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R;Gcdl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
Exigodl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
Exigodl, 16, 25-34, 1997
A;Title: Differential targetting of closely related ECM-glycoproteins: The pherophorin fit A;Reference number: Z17154; MUID:97162277; PMID:9009264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Redidues: 1-599 <COD>
A,Redidues: 1-599 <COD>
A,Redidues: 1-599 <COD>
A,Cross-references: UNIPROT: P93797; EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g165: A,Cross-references: UNIPROT: Bob_species Nagariensis
A,Experimental source: strain HR 10; sub_species Nagariensis
A,Note: in contrast to the other pherophorins, pherophorin-S is targeted to the cell-free C;Keywords: extracellular matrix; glycoprotein; pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endoglucanase C (EC 3.2.1.-) - Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Species: Cellulomonas fimi
C;Date: 3.1Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: 515271; A43636
R;Coutinho, J.B.; Moser, B.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
A;Title: Nucleotide sequence of the endoglucanase C gene (cenC) of Cellulomonas fimi, it: A;Reference number: $15271; MUID:92065819; PMID:1956299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                     C.Species: Drosophila melanogaster
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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R;D.Henderson, K.; J.Andrew, D.
Biochem. Biophys. Res. Commun. 252, 195-201, 1998
A;Title: Identification of a novel Drosophila SMAD on the X chromosome.
A;Reference number: JE0341; MUID:99032828; PMID:9813169
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C;Superfamily: human transcription regulator MAD-4
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A;Molecule type: DNA
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C;Superfamily: human transcription regulator MAD-4
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   Mismatches
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Query Match Best Local Similarity 100.v The 6; Conservative

1 TPPPGY 6

1-467 <ZHA>

A; Molecule type: mRNA

A;Residues:

216 TPPPGY 221

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1 TPPPGY 6

Best Local Similarity Matches 6; Conserv

us-09-385-918-18.rpr

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89.7%;
          Query Match
Best Local Similarity 83.3.
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - carrot
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142 SPPPGY 147
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C;Species: GlyCtine max (soybean)
C;Species: GlyCtine max (soybean)
C;Date: 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S33621
R;Datta, N.; LaFayette, P.R.; Kroner, P.A.; Nagao, R.T.; Key, J.L.
Plant Mol. Biol. 21, 859-869, 1993
A;Title: Isolation and characterization of three families of auxin down-regulated cDNA c
A;Reference number: S33620; MUID:93222483; PMID:8096772
A;Return preliminary
A;Molecule type: mRNA
A;Residues: 1-151 <DAT>
A;Cross-references: UNIPROT:Q06763; EMBL:X69640; NID:g296442; PIDN:CAA49341.1; PID:g2964
C;Genetics:
A;Gene: ADR11
C;Superfamily: hydroxyproline-rich glycoprotein
A; Residues: 1-1101 <COU>
A; Cross-references: UNIPROT: P14090; EMBL: X57858; NID: 948847; PIDN: CAA40993.1; PID: 958098
A; Cross-references: UNIPROT: P14090; EMBL: X57858; NID: 948847; PIDN: CAA40993.1; PID: 958098
A; Noder, B.; Gilkes, N.R.; Kilburn, D.G.; Warren, R.A.J.; Miller Jr., R.C.
Appl: Environ. Microbiol. 55, 2480-2487; 1989
A; Title: Purification and characterization of endoglucanase C of Cellulomonas fimi, clor A; Reference number: A43636; MUID: 90103465; PMID: 2604391
A; Reference region: A44536
A; Status: preliminary
A; Residues: 1-64, W, <MOS>
A; Cross-references: GB: M29707; NID: 9144417; PIDN: AAA23087.1; PID: 9144420
C; Genetics:
A; Gene: cenC
A; Statt codon: GTG
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F26H11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T21432
Subatte: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21432
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19421
A;Accession: T21432
A;Accession: T2432
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A;Map position: 2
A;Introns: 56/3; 154/2; 373/2; 417/3; 505/2; 596/1; 703/2; 847/3; 922/3; 1034/2; 1078/2;
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100.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 0; Indels
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1e+02;
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100.0%; Pred. No. 1e+
tive 0; Mismatches
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Best Local Similarity 100.
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Best Local Similarity
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probable cell wall-plasma membrane linker protein PRP precursor - rape N.Alternate names: hybrid-proline-rich protein C.Species: Brassica napus (rape) C.Species: Brassica napus (rape) C.Species: Brassica napus (rape) C.Species: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004 C.Spacession: 871558 R.Goodwin, W.; Pallas, J.A.; Jenkins, G.I. R.Goodwin, W.; Pallas, J.A.; Jenkins, G.I. A.Fitle: Transcripts of a gene encoding a putative cell wall-plasma membrane linker prot A;Reference number: 871558; MUID:96400032; PMID:8806408 A;Accession: 871558
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C,Superfamily: hydroxyproline-rich glycoprotein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-376/Product: probable cell wall-plasma membrane linker protein PRP #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: Daucus carota (carrot)
Cispecies: Daucus carota (carrot)
Cispate: 20.Sep.1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
Cispate: 20.Sep.1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30764
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss,
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A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Modecule type: mRNA
A, Residues: 1-347 «KAW»
A, Residues: 1-347 «KAW»
A, Ross-references: UNIPROT: P93705; EMBL: AB000505
A, Cross-references: cultivar Kurodagosun; hypocotyl
C, Superfamily: hydroxyproline-rich glycoprotein
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83.3%; Pred. No. 1.5e+02;
ive 1; Mismatches 0;
DB 2;
59;
Score 35; DB
Pred. No. 59;
1; Mismatches
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Search completed: October 13, 2005, 15:11:27 Job time : 4.50549 secs
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AD1863
cobalamin biosynthesis precorrin-3 methylase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Species: Nostoc sp. strain PCC 7120
C;Accession: AD1863
C;Accession: AD1863
C;Accession: AD1863
C;Accession: AD1863
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Triguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DN Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Status: Preliminary
A; DN A;
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: 220876; MUID:96325459; PMID:8670425
A;Accession: T30764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-532 <SEN>
A;Crosser-references: UNIPROT:Q98328; EMBL:U60315; PIDN:AAC55290.1
C;Genetics:
A;Note: MC162R
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A;Experimental source: strain PCC 7120
A;Genetics:
A;Genetics: all0453
C;Superfamily: Bifunctional CbiG/precorrin methyltransferase
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C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15046
R;Nakakita, M.
Submitted to the EWBL Data Library, April 1998
A;Description: Putative cDNA for arginine decarboxylase from Nicotiana sylvestris.
A;Accession: T15046
A;Ceros: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-621 cNAK>
A;Cross:references: UNIPROT:O64453; EMBL:AB012873
C;Genetics:
A;Gene: ACC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 35; DB 2; Length 574;
83.3%; Pred. No. 2.3e+02;
Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.7%; Score 35; DB 2; Length 532;
83.3%; Pred. No. 2.1e+02;
ive 1; Mismatches 0; Indels
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Best Local Similarity 83.30,
Fines 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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139 SPPPGY 144
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121 TPPPGF 126
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Cibate: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
Cibate: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
Cibacession: T1525
Submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
A;Accession: T1525
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-711 - WAMN
A;Residues: 1-711 - WAMN
A;Residues: UNIPROT: Q9Y409; EMBL: AL080140
A;Experimental source: adult testis; clone DKFZp431243
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                                                    Gaps
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  Length 621;
Score 35; DB 2; Length 621
Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          hypothetical protein DKFZp434L243.1 - human (fragment)
Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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October 13, 2005, 14:03:23; Search time 11.4286 Seconds (without alignments) 268.842 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                              Run on:
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US-09-385-918-18 39

1 TPPPGY 6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues

1612378 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Q8wny3 ovis aries	Q887p0 pseudomonas		Q8mkc6 ovis aries	Q96232 asparagus o	_		m				gallus gal		Q66hx9 brachydanio	brach		5 mus m	P84024 sus scrofa	P84025 rattus norv	Q90ye5 xenopus lae	Q68ep5 xenopus tro	'n	P84023 gallus gall	O66156 streptomyce	_	034662 bacillus su	Q8t8c9 halocynthia		2 arabi	5 homo	Q62432 mus musculu
ID	QBWNY3	Q887P0	Q864T4	QBMKC6	Q96232	Q8VWX9	Q94EV4	023583	Q86NL2	Q919P1	070112	Q919P2	Q6QAN7	6хн990	Q8AY16	SMA3_HUMAN	SMA3 MOUSE	SMA3_PIG	SMA3_RAT	Q90YE5		_	SMA3_CHICK	066156	Q6VP00	YODT BACSU	Q8T8 <u>C</u> 9	Q7PK45	Q8L7L2	SMA2_HUMAN	SMA2_MOUSE
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Score	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
Result No.	T	8	e	4	ហ	φ	7	<b>8</b> 0	o	10	11	12	13	14	15	16	. 17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

O70436 rattus norv OBUWÉ3 gallus gall O91912 xenopus lae O61919 brachydanio O64018 brachydanio O64018 brachydanio O91018 brachydanio O91018 brachydanio O91018 brachydanio O91018 brachydanio O91019 drosophila O6601 drosophila O6601 orosophila O66177 Osymbiobacte P93797 volvox cart O85017 oryza sativ	,	te) ta; Euteleostomi; Pecora; Bovidae;	Combarnous Y., and L T2 Gonadotrope
SMA2_RAT QBUWF3 QBUWF3 Q91912 Q61912 Q618R4 1 G6GNB Q72U35 Q72U35 Q72U35 Q72U35 Q97ZQ2 Q6660 Q6600 Q69UCS Q69177 Q850T7	ALIGNMENTS PRT; 77 AA.	el. 20, Created) el. 20, Last sequence update) el. 20, Last annotation update) Chordata; Craniata; Vertebrata; Cetartiodactyla; Ruminantia; Pec	iman A., Canepa S., s in Ovine Pituitary (2003).
99 100.0 99 100.0 90 100	PRELIMINARY;	EMBLr EMBLr EMBLr ). ep). zoa; ria;	; .A. illy ing ing 8:18 AAL
WWWWWWWWWWWWWW	RESULT 1 QBWNY3 ID QBWNY3		NCBI_TAXID=9940 RN FIJ RN SEQUENCE FROM N RX PubMed=12606325 RA TAYAGATE (; reclair re

ö Gaps Pseudomonas syringae (pv. tomato). Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. NCBI\_TaxID=323; ; 0 100.0%; Score 39; DB 2; Length 77; 100.0%; Pred. No. 43; tive 0; Mismatches 0; Indels 77 AA; 8356 MW; 798FDA37ACE78781 CRC64; Q887P0; 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein. OrderedLocusNames=PSPT01251; 125 AA. PRT; Query Match 100. Best Local Similarity 100. Matches 6, Conservative PRELIMINARY; ||||||| | TPPPGY 55 1 TPPPGY 6 77 NON TER NON TER SEQUENCE 20 Q887P0 RESULT 2

ò g SEQUENCE FROM N.A.
STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,

AC DOT DOT DOT SERVING SERVING

171 AA.

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01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, Smad3 (Fragment).
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Matches 6; Conservative
      PRELIMINARY;
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Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000."; Prosec. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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PubMed=12606325;
Dupont J., McNeilly J., Vaiman A., Canepa S., Combarnous Y.,
Taragnat C.;
"Activin Signaling Pathways in Ovine Pituitary and L T2 Gonadotrope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smad2 (Fragment).
Ovis aries (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001132; Dwarfin A.
InterPro; IPR008994; SMAD_FHĀ.
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                                                                                                                                                                                                                                                                                                                                          100.0%; Score 39; DB 2; Length 125; 100.0%; Pred. No. 72;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                         Complete proteome, Hypothetical protein.
SEQUENCE 125 AA; 13851 MW; 450717203FF6205B CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY185300; AAO27459.1; -.
HSSP; Q15796; 1DEV.
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أحمد 6; Conservative
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Matches 6; Conservative
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Pfam; PF03166; MH2; 1.
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72 TPPPGY 77
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83 TPPPGY 88
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096212;
01-FBB-1997 (TYEMBLrel. 02, Created)
01-FBB-1997 (TYEMBLrel. 02, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Proline-rich-like protein.
Asparagus officinalis (Garden asparagus).
Bukaryota; Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
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                                                                                                                                                             Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO0132; DWarfin.
InterPro; IPRO08984; SMAD_FHA.
Pfam; PF03166; MH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                  Souza C.J.H., Baird D.T.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS08024; AAM34245.1; -.
HSSP; Q15796; 1DEV.
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Last annotation update)
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plant Cell Physiol. 37:706-710(1996)
EMBL; X82413; CAA57810.1; -.
HSSP; P24337; 1HYP.
InterPro; IPR003542; AAI.
Pfem; PR00234; Tryp_alpha_amyl; 1.
SWART; SM00499; AAI; 1.
PRT;
                                                             Created)
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PRELIMINARY;
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Q86NL2
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                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays (Maize).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=21664393; PubMed=11792865;
Fu H., Zheng Z., Dooner H.K.;
"Recombination rates between adjacent genic and retrotransposon regions in maize vary by 2 orders of magnitude.";
Proc. Natl. Acad. Sci. U.S.A. 99:1082-1087 (2002).

EMBL; AF931808; AAK73107.1; -..
InterPro; IPR007321; Transposase_28.

Fam: PF04195; Transposase_28; I.
SEQUENCE 254 AA; 28236 MW; 2CECF606583C2BBB CRC64;
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                                                                                                                                                                                                                                                                                        TISSUE-Male and female floral buds;
TISSUE-Male and female floral buds;
Kahana A., Silberstein L., Kessler N., Perl-Treves R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF104392; AAL35979.1; -.
HSSP; P24337; 1HYP.
Pfam; PP00234; Tryp_alpha_amyl; 1.
SMATT; SM00499; AAI; 1.
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100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 AA; 22299 MW; 152B165EDA4A6F20 CRC64;
                                                                          (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
RIRE2 orf3.
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                                       219 AA
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                                         PRT;
                                                                                                                                   Extensin-like protein (Fragment).
                                                                                                                                                                             Cucumis sativus (Cucumber).
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Matches 6; Conservative
                                         PRELIMINARY;
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                                         Q8VWX9
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RESULT 6
Q8VWX9
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Q94EV4
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DT 01-JAN-1998 (TERMELEL, 05, Late sequence update)

DE MODICALE AND STREMELEL, 05, Late sequence update)

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DE MODICALELAL DICEBLE GLASS (REQUIRED TO THE ADDITION)

SANDELELAL DISTANCES AND STREME AND STREME AND STREET TRACHEOPHYES;

OCC SERMINOPHYES, WASHINGTHAN STREET TRACHEOPHYES;

NA KRESS M., KANANDAY T., BRIGHT K., RIGGER M., James H. M., MAIDH ST., CALL DAN STREET TRACHEOPHYES;

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A DOMEST OF THE MODICAL STREET TRACHEOPHYES;

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SEQUENCE FROM N.A.
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Q6QAN7;
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Q919P2
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Q6QAN7
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A Szendro P.I., Grunenberg U., Eichele G.;
Szendro P.I., Grunenberg U., Eichele G.;
Szendro P.I., Grunenberg U., Eichele G.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

BMBL; AF230191; AAF36971.1; -.

R HSSP; Q15796; 1DEV.

R TRANSPAC; T04248; -.

R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001132; Dwarfin A.

R InterPro; IPR008984; SMAD_FHĀ.

R InterPro; IPR008984; SMAD_FHĀ.

R Pfam; PF03165; MH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 15, Last sequence update)
TGF-beta response effector Smad3 (Fragment).
Gallus gallus (Chicken).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AGCP8800.
Name=agGG55075; ORFNames=ENSANGG0000013217;
Anopheles gambiae str. PEST.
BUKAryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NBI_TAXID=180454;
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                                                                                                                                                                                                                                                                   100.0%; Score 39; DB 2; Length 308; 100.0%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                0; Indels
GO; GO:0016319; P:mushroom body development; IMP.
GO; GO:0007476; P:Wing morphogenesis; IMP.
InterPro; IPR001132; Dwarfin.
InterPro; IPR008984; SMAD_FHA.
Ffam; PF03166; MH2; 1.
SMART; SM0654; DMB; 1.
SEQUENCE 308 AA; 33197 MW; 16FBA0E476E501CB CRC64;
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Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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SMART; SM00524; DWB; 1.
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74 TPPPGY 79
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(2919P)
AC 0919P
DT 01-0C
DT 01-0C
DT 01-0C
DE TGF-b
DE TGF-b
OC Archo
OC Archo
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DR RA SZEUGH
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DR RASSP;
DR HSSP;
DR TRANS;
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Q7Q112
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
TGF effector Smad2 (Fragment).
TGF effector Smad2 (Fragment).
Ealbas gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Szendro P.I., Eichele G.;
Szendro P.I., Eichele G.;
Submitted (JAN-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AF230190; AAF36969.1; -.
HSSP; Q15796; IKHX.
HSSP; Q15796; T04247; -.
G0; G0:0005422; C:intracellular; IEA.
G0; G0:000555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR003619; Dwarfin.
InterPro; IPR003619; Dwarfin.
InterPro; IPR008984; SMAD_FHĀ.
                                                                                                                                                             HSSP; Q15796; IDBV.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0006352; C:intracellular; IEA.
InterPro; IPR003132; Dwarfin.
InterPro; IPR003619; Dwarfin. A.
InterPro; IPR003694; SWAD_FHĀ.
Pfam; PF03165; MH1; 1.
Pfam; PF03165; MH2; 1.
Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBunk/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAAB01008980; EAA13835.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                      378 AA; 42530 MW; AEF8ED24C03777F1 CRC64;
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Best Local Similarity 100.C
Matches 6; Conservative
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Best Local Similarity 100.0
Matches 6; Conservative
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SMART; SM00524; DWB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03165; MH1; 1.
Pfam; PF03166; MH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 TPPPGY 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TPPPGY 6
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completed: October 13, 2005, 15:09:29
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Job time: 12.4286 secs
     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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TISSUE-Whole:

Tataubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatchenco L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raheloy D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Anting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rrzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse Chan Sections on and initial analysis of more than 15,000 full-length human
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005622; C:intracellular; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                               Lau M.T., Ge W.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 AA; 47751 MW; 043A37DACADE1F2D CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MAD, mothers against decapentaplegic homolog 3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001132; Dwarfin.
InterPro; IPR003619; Dwarfin A.
InterPro; IPR008984; SMAD_FHĀ.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY550113; AAS57862.1; -.
                                                                                                                 Carassius auratus (Goldfish).
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Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00523; DWA; 1.
SMART; SM00524; DWB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03165; MH1; 1.
Pfam; PF03166; MH2; 1.
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176 TPPPGY 181
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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25-OCT-2004
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066HX9
10 66HX9
10 66HX9
10 66HX9
10 66HX9
10 66HX9
10 725-0C
10 7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00132; Dwarfin A.
InterPro; IPR001894; SWAD_FHĀ.
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                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Score 39; DB 2; Length 423; Similarity 100.0%; Pred. No. 2.7e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 39; DB 2; Length 423; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22105668; PubMed=12112463; DOI=10.1002/dvdy.10113;
Pagoda H.M., Meyr. D.;
"Zebrafish Smad7 is regulated by Smad3 and BMP signals.";
Dev. Dyn. 224:334-349(2002).
Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC081628, AAH81628.1;
Interpro; IPR001132; Dwarfin.
Interpro; IPR003619; Dwarfin.
Interpro; IPR008694; SMAD_FHĀ.
Pfam; PF03166; MH1; 1.
SMART; SM00523; DWA; 1.
SMART; SM00524; DWA; 1.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY134490; AAN08604.1; --
HSSP; OLS'96: 1DEV.
ZFIN; ZDB-GENE-030128-4; smad3b.
                                                                                                                                                                                                                                                                       423 AA; 47733 MW; DB9092893AC77471 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Smad3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=smad3b; Synonyms=madh3b;
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 AA
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ses 6; Conservative
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Pfam; PF03166; MH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 TPPPGY 182
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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